

US-08-702-525-22

Query Match	30.6%;	Score 110;	DB 4;	Length 1120;
Best Local Similarity	73.5%;	Pred. No. 2.6e-25;		
Matches 169; Conservative	0;	Mismatches 55;	Indels 6;	Gaps 2

Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

OY 1 ATACAGGTATCCCGAACCCTAAGAGATGTAATTTTCAGCTAAACACTGAGAATTCACT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 584 ATACAGGTTACCCAGAACCTAAGAGATGATGTTTGGCTAAGAACCAAGAATTCACT 643

61 ACTAGTATGACTGTCATGAAGAAATCTCAAATATGTGACGAACTGTACAAAGTT 120

Db 644 ATCGAGTATGATGGTATTATGCAGAACTCTCAGATAATGTCACAGAACTGTACGACGTT 703

Db 704 TCCATCAGCTTGCTCTGTTTCATTCCCTGATGTTACGAGCAATATGACCATCTTCTGATT 763

1/8 CIGAAACCGAGACACTGGAGATGCTGGCTCTCCCTACCTTTCAATATAGA 227

Db 764 CTGGAACCTGACA - - ACACCGCGGCTTTATCTTCACCTTCTCTATAGA 810

Search completed: October 19, 2002, 23:36:15
Job time : 17.4407 sec

Job time : 17.4497 secs

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;
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,744A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/280,757
; FILING DATE: 26-JUL-1994
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 28-AUG-1993
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-479-744A-1

Query Match 30.6%; Score 110; DB 3; Length 1120;
Best Local Similarity 73.5%; Pred. No. 2.6e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAAGGTTGCCAGACCTAGAGATGATTTTCAGCTAAACCTGAGAAATTCACCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 ATACAGGTTGCCAGACCTAGAGATGATTTTCAGCTAAACCTGAGAAATTCACCT 643
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACACGTT 120
    | ||||| | | | | | ||||| ||||| ||||| ||||| ||||| |||||
DB 644 ATCGAGTATGATGATTTATTCAGAAATCTCAAGATATATGTCACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCCCTTTTCAGTCCCTGAG--CACACATGTGAGCGCTTTGTGCC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 704 TCCATCAGCTTGCTGTTTATTCCTCGATGTTTACGAGCAATATGACCATTTCTGTATT 763
QY 178 CTGAAACTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 764 CTGAAACTGACA--AGACGGCGCTTTTATCTTCACCTTCTCTATAGA 810

RESULT 13
US-08-280-757B-1
; Sequence 1, Application US/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: NO. 6130316el CT144/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,757B
; FILING DATE: 26-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-280-757B-1

Query Match 30.6%; Score 110; DB 3; Length 1120;
Best Local Similarity 73.5%; Pred. No. 2.6e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAAGGTTGCCAGACCTAGAGATGATTTTCAGCTAAACCTGAGAAATTCACCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 ATACAGGTTGCCAGACCTAGAGATGATTTTCAGCTAAACCTGAGAAATTCACCT 643
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACACGTT 120
    | ||||| | | | | | ||||| ||||| ||||| ||||| ||||| |||||
DB 644 ATCGAGTATGATGATTTATTCAGAAATCTCAAGATATATGTCACAGAACTGTACACGTT 703
QY 121 TCTATCAGCTTGCCCTTTTCAGTCCCTGAG--CACACATGTGAGCGCTTTGTGCC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 704 TCCATCAGCTTGCTGTTTATTCCTCGATGTTTACGAGCAATATGACCATTTCTGTATT 763
QY 178 CTGAAACTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
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DB 764 CTGAAACTGACA--AGACGGCGCTTTTATCTTCACCTTCTCTATAGA 810

RESULT 14
US-08-205-697A-22
; Sequence 22, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: NO. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
```

```

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
;
; US-08-456-104-1
;
; Query Match 30.6%; Score 110; DB 2; Length 1120;
; Best Local Similarity 73.5%; Pred. No. 2.6e-25;
; Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
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; QY 1 ATACAGGTTACCCAGACCTAAGAGATGTTTTCAGCTAAACCTGAGATTCACT 60
; DB 584 ATACAGGTTACCCAGACCTAAGAGATGAGTGTGTTTCTAAGAACCAAGATTCACT 643
; QY 61 ACTAAGTATGATGTGTCATGAGAAATCTCAAAATATATGTGACAGACTGTACAAAGTT 120
; DB 644 ATGAGATATGATGTATTTATGCAAGAAATCTCAAGATTAATGTACAGAACTGTACAGCGTT 703
; QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
; DB 704 TCCATCAGCTTGCTGTTCATTCCTGATGTACGAGCAATATGACCACTTCTGTAT 763
; QY 178 CTGAACCTGAGACACTGAGATGCTGCTGCCCTACCTTTCAATATAGA 227
; DB 764 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAGA 810
;
; RESULT 11
; US-08-101-624-1
; Sequence 1, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD

```

```

; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
;
; US-08-101-624-1
;
; Query Match 30.6%; Score 110; DB 2; Length 1120;
; Best Local Similarity 73.5%; Pred. No. 2.6e-25;
; Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;
;
; QY 1 ATACAGGTTACCCAGACCTAAGAGATGATGTTTTCAGCTAAACCTGAGATTCACT 60
; DB 584 ATACAGGTTACCCAGACCTAAGAGATGAGTGTGTTTCTAAGAACCAAGATTCACT 643
; QY 61 ACTAAGTATGATGTGTCATGAGAAATCTCAAAATATATGTGACAGACTGTACAAAGTT 120
; DB 644 ATGAGATATGATGTATTTATGCAAGAAATCTCAAGATTAATGTACAGAACTGTACAGCGTT 703
; QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
; DB 704 TCCATCAGCTTGCTGTTCATTCCTGATGTACGAGCAATATGACCACTTCTGTAT 763
; QY 178 CTGAACCTGAGACACTGAGATGCTGCTGCCCTACCTTTCAATATAGA 227
; DB 764 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAGA 810
;
; RESULT 12
; US-08-479-744A-1
; Sequence 1, Application US/08479744A
; Patent No. 6084067
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; City: Boston
; STATE: Massachusetts

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US-09-039-641-33
 : Sequence 33, Application US/09039641
 : Patent No. 6251627
 : GENERAL INFORMATION:
 : APPLICANT: Cal, Zeling
 : APPLICANT: Sprent, Jonathan
 : APPLICANT: Brumark, Anders
 : APPLICANT: Jackson, Michael
 : APPLICANT: Peterson, Per A.
 : APPLICANT: Peterson, Michael
 : TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
 : TITLE OF INVENTION: ACTIVATION OF T-CELLS
 : NUMBER OF SEQUENCES: 45
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Olson & Hierl, Ltd.
 : STREET: 20 No. 6251627th Wacker Drive, Suite 3000
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: USA
 : ZIP: 60606
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/039,641
 : FILING DATE: 8-MAR-1995
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Olson, Arne M.
 : REGISTRATION NUMBER: 30,203
 : REFERENCE/DOCKET NUMBER: TSRI4710
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (312) 580-1180
 : TELEFAX: (312) 580-1189
 : INFORMATION FOR SEQ ID NO: 33:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1002 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : HYPOTHEICAL: NO
 : ANTI-SENSE: NO
 : US-09-039-641-33

Query Match 30.6%; Score 110; DB 4; Length 1002;
 Best Local Similarity 73.5%; Pred. No. 2.5e-25;
 Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTATCCAGAACCTTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 60
 DB 484 ATACAGGTTATCCAGAACCTTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 543
 QY 61 ACTAAGTATGATGCTGATGAGAAATCTCAAAATTAATGACAGAACTGTACAGCTT 120
 DB 544 ATCGAGTATGATGATGATATGCAAGAAATCTCAAGATTAATGACAGAACTGTACAGCTT 603
 QY 121 TCTATCAGTTCGCTTTTTCAGTCCCTGAG---CACACAATGAGAGGCTCTTTGTGCC 177
 DB 604 TCCATCAGTTCGCTTTTTCAGTCCCTGATGTTACGAGCAATATACCATCTTCTGTATT 663
 QY 178 CTGAACCTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
 DB 664 CTGGAACCTGACA---AGACGGGCTTTTATCTTACCTCTTCTATAGA 710

RESULT 9
 US-09-039-762A-33
 : Sequence 33, Application US/09039762A
 : Patent No. 6255073
 : GENERAL INFORMATION:
 : APPLICANT: Cal, Zeling

APPLICANT: Sprent, Jonathan
 APPLICANT: Brumark, Anders
 APPLICANT: Jackson, Michael
 APPLICANT: Peterson, Per A.
 APPLICANT: Peterson, Michael
 TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
 TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Olson & Hierl, Ltd.
 STREET: 20 No. 6255073th Wacker Drive, 36th Floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/039,762A
 FILING DATE: 16-MAR-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Olson, Arne M.
 REGISTRATION NUMBER: 30,203
 REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 580-1180
 TELEFAX: (312) 580-1189
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1002 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-09-039-762A-33

Query Match 30.6%; Score 110; DB 4; Length 1002;
 Best Local Similarity 73.5%; Pred. No. 2.5e-25;
 Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTATCCAGAACCTTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 60
 DB 484 ATACAGGTTATCCAGAACCTTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 543
 QY 61 ACTAAGTATGATGCTGATGAGAAATCTCAAAATTAATGACAGAACTGTACAGCTT 120
 DB 544 ATCGAGTATGATGATGATATGCAAGAAATCTCAAGATTAATGACAGAACTGTACAGCTT 603
 QY 121 TCTATCAGTTCGCTTTTTCAGTCCCTGAG---CACACAATGAGAGGCTCTTTGTGCC 177
 DB 604 TCCATCAGTTCGCTTTTTCAGTCCCTGATGTTACGAGCAATATACCATCTTCTGTATT 663
 QY 178 CTGAACCTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
 DB 664 CTGGAACCTGACA---AGACGGGCTTTTATCTTACCTCTTCTATAGA 710

RESULT 10
 US-08-456-104-1
 : Sequence 1, Application US/08456104
 : Patent No. 5861310
 : GENERAL INFORMATION:
 : APPLICANT: Freeman, Gordon J.
 : APPLICANT: Nadler, Lee M.
 : APPLICANT: Gray, Gary S.
 : TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:

Db 544 ATGAGATATGATGATATGAGAAATCTCAGATATATGTCAGAACTGATGACGCT 603
QY 121 TCTATGAGCTTGCCTTTTATGATCCCTGAG--CACAAGATGAGGCTCTTTTGTGC 177
Db 604 TCCATGAGCTTGTCTGTTTATTCCTGATTTACGAGAAATGACATCTCTGTAT 663
QY 178 CTGAAGTGGAGACATGCTGCTGCTCTCTACTCTTCAATATAGA 227
Db 664 CTGAAGTGGAGACATGCTGCTGCTCTCTACTCTTCAATATAGA 710

RESULT 6
US-08-848-760B-11
Sequence 11, Application US/08848760B
Patent No. 6248721

GENERAL INFORMATION:

APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: United States of America
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/838,702
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-848-760B-11

Query Match 30.6%; Score 110; DB 4; Length 972;
Best Local Similarity 73.5%; Pred. No. 2.5e-25;

Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTACGCTAAACACTGGAATTCAC 60
Db 460 ATACAGGTTACCCAGAACCTAAGAGATGATTTTACGCTAAACACTGGAATTCAC 519
QY 61 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 520 ATCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
QY 121 TCTATGAGCTTGCCTTTTATGATCCCTGAG--CACAAGATGAGGCTCTTTTGTGC 177
Db 580 TCTATGAGCTTGCCTTTTATGATCCCTGAG--CACAAGATGAGGCTCTTTTGTGC 639

QY 178 CTGAAGTGGAGACATGCTGCTGCTCTCTACTCTTCAATATAGA 227
Db 640 CTGAAGTGGAGACATGCTGCTGCTCTCTACTCTTCAATATAGA 686

RESULT 7
US-09-039-982A-33
Sequence 33, Application US/09039982A
Patent No. 6225042

GENERAL INFORMATION:

APPLICANT: Cal, Zelling
APPLICANT: Sprent, Jonathan
APPLICANT: Brummark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hiern, Ltd.
STREET: 20 No. 6225042th Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,982A
FILING DATE: 16-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-982A-33

Query Match 30.6%; Score 110; DB 4; Length 1002;
Best Local Similarity 73.5%; Pred. No. 2.5e-25;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTACGCTAAACACTGGAATTCAC 60
Db 464 ATACAGGTTACCCAGAACCTAAGAGATGATTTTACGCTAAACACTGGAATTCAC 543
QY 61 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 544 ATCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
QY 121 TCTATGAGCTTGCCTTTTATGATCCCTGAG--CACAAGATGAGGCTCTTTTGTGC 177
Db 604 TCTATGAGCTTGCCTTTTATGATCCCTGAG--CACAAGATGAGGCTCTTTTGTGC 663
QY 178 CTGAAGTGGAGACATGCTGCTGCTCTCTACTCTTCAATATAGA 227
Db 664 CTGAAGTGGAGACATGCTGCTGCTCTCTACTCTTCAATATAGA 710

RESULT 8

[illegible]

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RESULT 5
US-09-039-762A-34
: Sequence 34, Application US/09039762A
: Patent No. 6255073
:
: GENERAL INFORMATION:
: APPLICANT: Cal, Zelig
: APPLICANT: Sprent, Jonathan
: APPLICANT: Brummark, Anders
: APPLICANT: Jackson, Michael
: APPLICANT: Peterson, Per A.
: TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
: TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
: NUMBER OF SEQUENCES: 59
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Olson & Hjerl, Ltd.
: STREET: 20 No. 6255073th Wacker Drive, 36th Floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/039,762A
: FILING DATE: 16-MAR-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OLSON, Arne M.
: REGISTRATION NUMBER: 30,203
: REFERENCE/DOCKET NUMBER: TSHI 471.0 DIV.2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 580-1180
: TELEFAX: (312) 580-1189
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 751 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
:
: US-09-039-762A-34
:
: Query Match 30.6%; Score 110; DB 4; Length 751;
: Best Local Similarity 73.5%; Pred. No. 2, 2e-25;
: Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2
:
: 1 ATACAGGTTAACCACACCTAAGAGATGTATTTTCACGTAACAACCTGAGATTCAACT 60
: ||||| ||||||| ||||||| ||||| || ||||| || |||||||
: Db 484 ATACAGGTTAACCACACCTAAGAGATGTATTTTCACGTAACAACCTGAGATTCAACT 543
:
: 51 ATACAGGTTAACCACCTGCTGTAAGCAATATTCGAAATAAATGTCGACAACTGTACAGGTT 120

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STRANDEDNESS: single

ANTI-SENSE:
US-09-039-982A-34

ANTI-SENSE:
US-09-039-982A-34

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 : Search time 12.4497 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggtaccagacc.....ggcgacaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCOTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	30.6	306	3 US-08-479-744A-46	Sequence 46, Appl
2	110	30.6	306	3 US-08-280-757B-46	Sequence 46, Appl
3	110	30.6	751	4 US-09-039-982A-34	Sequence 34, Appl
4	110	30.6	751	4 US-09-039-641-34	Sequence 34, Appl
5	110	30.6	751	4 US-09-039-762A-34	Sequence 34, Appl
6	110	30.6	972	4 US-08-848-760B-11	Sequence 11, Appl
7	110	30.6	1002	4 US-09-039-982A-33	Sequence 33, Appl
8	110	30.6	1002	4 US-09-039-641-33	Sequence 33, Appl
9	110	30.6	1002	4 US-09-039-762A-33	Sequence 33, Appl
10	110	30.6	1120	2 US-08-456-104-1	Sequence 1, Appl
11	110	30.6	1120	2 US-08-101-624-1	Sequence 1, Appl
12	110	30.6	1120	3 US-08-479-744A-1	Sequence 1, Appl
13	110	30.6	1120	3 US-08-280-757B-1	Sequence 1, Appl
14	110	30.6	1120	3 US-08-205-697A-22	Sequence 22, Appl
15	110	30.6	1120	4 US-08-702-525-22	Sequence 22, Appl
16	110	30.6	1120	4 US-08-403-253A-3	Sequence 3, Appl
17	110	30.6	1120	5 PCT-US95-02576-22	Sequence 22, Appl
18	110	30.6	1161	4 US-08-702-525A-24	Sequence 24, Appl
19	110	30.6	1161	4 US-08-702-525-24	Sequence 24, Appl
20	110	30.6	1161	5 PCT-US95-02576-24	Sequence 24, Appl
21	110	30.6	1424	4 US-09-326-186B-226	Sequence 226, App
22	110	30.6	1428	5 PCT-US94-09642-1	Sequence 1, Appl
23	110	30.6	210	4 US-08-205-697A-31	Sequence 31, Appl
24	78	21.7	210	4 US-08-702-525-31	Sequence 31, Appl
25	78	21.7	210	5 PCT-US95-02576-31	Sequence 31, Appl
26	77.2	21.5	1151	4 US-08-456-104-3	Sequence 3, Appl
27	77.2	21.5	1151	4 US-08-205-697A-20	Sequence 20, Appl

28	77.2	21.5	1151	4 US-08-702-525-20	Sequence 20, Appl
29	77.2	21.5	1151	5 PCT-US95-02576-20	Sequence 20, Appl
30	77.2	21.5	1163	3 US-08-479-744A-22	Sequence 22, Appl
31	77.2	21.5	1163	3 US-08-280-757B-22	Sequence 22, Appl
32	77.2	21.5	1261	4 US-08-205-697A-12	Sequence 12, Appl
33	77.2	21.5	1261	4 US-08-702-525-12	Sequence 12, Appl
34	77.2	21.5	1261	5 PCT-US95-02576-12	Sequence 12, Appl
35	31.2	8.7	740	4 US-09-342-681C-99	Sequence 213, App
36	30	8.4	1978	4 US-08-936-165A-213	Sequence 3, Appl
37	30	8.4	2351	4 US-09-276-531-3	Sequence 24, Appl
38	30	8.4	4865	3 US-08-894-017-24	Sequence 6, Appl
39	29.8	8.3	785	3 US-09-008-979A-6	Sequence 6, Appl
40	29.8	8.3	785	4 US-09-460-618-6	Sequence 1, Appl
41	29.6	8.2	2215	2 US-08-980-329C-1	Sequence 1, Appl
42	29.4	8.2	14683	3 US-08-819-866-1	Sequence 1, Appl
43	29.4	8.2	14683	2 US-09-023-715-1	Sequence 1, Appl
44	29.2	8.1	263	3 US-09-157-177-121	Sequence 121, App
45	29.2	8.1	1371	2 US-08-428-713-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-479-744A-46
Sequence 46, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

PS Claim 1; Page 121-123; 148bp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other;

Query Match 63.3%; Score 227.2; DB 20; Length 2830;
Best Local Similarity 94.8%; Pred. No. 4.1e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACACTGAGATTCAACT 60
DB 2169 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACACTGAGATTCAACT 2110
OY 61 ACTAAGTATGATGTCTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACAACTT 120
DB 2109 ACTAAGTATGATGTCTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACAACTT 2050
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGAGCGCTTTGTGCCCTG 180
DB 2049 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGAGCGCTTTGTGCCCTG 1990
OY 181 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGAACATCAAAAGG 240
DB 1989 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGATGACAACTAAG 1930
OY 241 GAGAGAAA 248
DB 1929 GATTAAGA 1922

RESULT 15
AAZ27915
ID AAZ27915 standard; DNA: 987 BP.
XX
AC AAZ27915;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2 protein coding sequence.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
OS
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
DR P-PSDB; AAY41076.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases

XX
PS Claim 1; Page 102-103; 148bp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match 47.2%; Score 169.4; DB 20; Length 987;
Best Local Similarity 87.2%; Pred. No. 3.4e-40;
Matches 198; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

OY 1 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACACTGAGATTCAACT 60
DB 481 ATACAGGTTACCCAGAACCTAAGAGATGTATTTTCAGCTAACACTGAGATTCAACT 540
OY 61 ACTAAGTATGATGTCTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACAACTT 120
DB 541 ACTAAGTATGATGTCTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACAACTT 600
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGAGCGCTTTGTGCCCTG 180
DB 601 TCTATCAGCTTGCCTTTTTCAGTCCGGAAGACACAAATGTGAGCGCTTTGTGCCCTG 660
OY 181 AAACCTGAGACACTGAGATGCTGCTCCCTACCTTTCAATATAGAA 227
DB 661 CAAGTGTAGTCAAT--GAAGCTTCCCTCCCTACCTTATATATAGA 704

Search completed: October 19, 2002, 23:33:38
Job time : 60.4731 secs

Query Match	63.3%	Score 227.2	DB 21	Length 1080
Best Local Similarity	94.8%	Pred. No. 2.9e-57		
Matches 235	Conservative 0	Mismatches 13	Indels 0	Gaps 0

RESULT 13	
AAZ27929	
ID	AAZ27929 standard; DNA; 2830 BP.

Feline B7-2 protein encoding DNA.

05 Felis catus.

PN W09947558-A2.

PD 23-SEP-1999.
yy

PF 19-MAR-1999; 99WO-US06187.
YY

PR 17-APR-1998; 98US-0062597.

PA (HESK-) HESKA CORP.

PI Sim G, Yang S, Sellins KS;
VY

DR WPI; 1999-571822/48.
DB P-PDDB; 22V41070

XX P-PSDB; AAY410/9.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
PT

PS Claim 1; Page 116-119; 148pp; English.

The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.

Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;

Query Match	63.3%;	Score 227.2;	DB 20;	Length 2830;
Best Local Similarity	94.8%;	Pred. No. 4.1e-57;		
Matches 235; Conservative	0;	Mismatches 13;	Indels 0;	Gaps 0

QY 1 ATACAGGTTACCCAGAACCTAAGGAGATGTATTTTCAGCTAAACACTGAGAATTCACCT 60

DD 662 ATACAGGTTACCCAGAACCTAAGGAGTGTATTTTCAGCTAAACACTGAGAATTCACCT 72]

01 ACIAAGTAAGTACCTGACGAAGAATCTCAAAATAATGTACAGAACCTGTACCAACGTT 120

22 122 AGGAGTGGATACCGTCCATGGAGAAACCTCAAAATAAAGTGACAGAACTGTACAAAGTT /81

[illegible]

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[illegible]

007 341 6666666 348

Dh 902 GATTAAGCA 909

RESULT 14

ID	AAZ27930 standard; DNA; 2830 BP.
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AC AAZ27930;
VY

DT 20-DEC-1999 (first entry)
XX

DE feline B/-2 gene complementary DNA sequence.

allergic reaction; infectious disease; tumor development: feline: KW
B/, C14A4; 1 cell costimulatory protein; dog; cat; autoimmune disease, KW

gland rejection, inflammation, arthritis, atrophic dermatitis; 55
XX

XX

XX

XX

XX

PR 17-APR-1998; 98US-0062597.

PA (HESK-) HESKA CORP.
YY

PI Sim G, Yang S, Sellins KS, XX

DK WFL; 1999-5/1822/48
XX

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases -

```

XX AA234838;
AC
XX 28-FEB-2000 (first entry)
DF
XX Feline CD86 (B7-2) cDNA.
DE
XX CD86; B7-2; feline; cat; recombinant virus; vaccine;
KM immunomodulator; tumour; cancer; therapy; ss.
XX
OS Felis domesticus.
XX
FH Key Location/Qualifiers
FT CDS 63..1052
FT /*tag= a
XX
XX WO957295-A1.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09504.
XX
XX 01-MAY-1998; 98US-0071711.
XX
XX (SCHE ) SCHERING-PLOUGH LTD.
PA (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX
XX Winslow BJ, Cochran MD;
XX
XX WPI: 2000-062155/05.
DR P-PSDB; AAY32285.
XX
PT Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines -
XX
XX Disclosure: Fig 3A; 230pp; English.
XX
XX This is the nucleotide sequence of cDNA coding for feline CD86
XX (B7-2). The cDNA was isolated from feline peripheral blood
XX mononuclear cell cDNA by PCR. Manipulating the expression of CD28
XX or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
XX regulates T cell proliferation and cytokine release. The invention
XX relates to a recombinant virus that contains at least one foreign
XX nucleic acid, inserted into a nonessential genomic region, that
XX encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
XX immunogenic fragments, and is expressed when the recombinant virus
XX is introduced into a suitable host. The invention also provides:
XX a recombinant virus further comprising a foreign nucleic acid
XX encoding an immunogen derived from a feline pathogen; recombinant
XX viruses capable of enhancing an immune response to protect against
XX disease; recombinant viruses expressing antisense sequences;
XX capable of suppressing an immune response in a feline; e.g. for
XX treatment of autoimmune disease or transplant rejection; and
XX recombinant viruses expressing DNA encoding CD80 and/or CD86 used
XX to reduce or eliminate a tumour in cats.
XX
XX Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
SO
Query Match 63.3%; Score 227.2; DB 21; Length 1080;
Best Local Similarity 94.8%; Pred. 2.9e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATACAGGTTACCCAGACCTAGAGATGATTTTTCAGTAAACCTGAGAAATTCACACT 60
DB 546 ATACAAGTTACCCAGACCTAGAGATGATTTTTCAGTAAACCTGAGAAATTCACACT 605
QY 61 ACTAAGTATGATATGTCATGAAGAATTCATAAATAATGTCAGACAACTGACAAAGCTT 120
DB 606 ACTAAGTATGATATGTCATGAAGAATTCATAAATAATGTCAGACAACTGACAAAGCTT 665
QY 121 TCTATCAGTTCGCTTTTTCACCTCCCTGAGACACAACTGAGAGGCTCTTTTGCCCTG 180
DB 666 TCTATCAGTTCGCTTTTTCACCTCCCTGAGACACAACTGAGAGGCTCTTTTGCCCTG 725

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QY 181 AAACGAGACACTGGAGATGCTGCTCTCCCTACCTTTCATATAGAACATCAAAAGC 240
DB 726 AAACGAGACACTGGAGATGCTGCTCTCCCTACCTTTCATATAGAACATCAAAAGC 785
QY 241 GAGAGAAA 248
DB 786 GATTAAGA 793
RESULT 12
AA234785
ID AA234785 standard; cDNA; 1080 BP.
XX
XX AA234785;
AC
XX
XX 15-FEB-2000 (first entry)
XX
XX Cat CD86 (B7-2) cDNA.
DE
XX
XX CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
KM FIV; feline leukaemia virus; feline infectious peritonitis virus;
KM feline panleukopenia virus; feline calicivirus; feline reovirus-3;
KM feline rotavirus; feline coronavirus; feline syncytial virus;
KM feline sarcoma virus; feline herpesvirus; feline borna disease;
KM rabies virus; chlamydia; toxoplasmosis gondii; Dirofilaria immitis;
KM parasite; autoimmune disease; transplant rejection; therapy; ss.
XX
XX Felis domesticus.
XX
XX Key Location/Qualifiers
FH CDS 63..1052
FT /*tag= a
XX
XX WO957271-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09502.
XX
XX 01-MAY-1998; 98US-0071699.
XX
XX (TEXA ) TEXAS A & M SYSTEM.
XX
XX Collison EW, Hash SM, Choi I;
XX
XX WPI: 2000-052972/04.
DR P-PSDB; AAY32278.
XX
XX Novel feline proteins used to produce feline vaccines which prevent
XX infectious disease or to promote growth in homologous or heterologous
XX species -
XX
XX Claim 6; Fig 3A; 186pp; English.
XX
XX This is the nucleotide sequence of cDNA encoding feline CD86
XX (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
XX peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
XX comprising nucleic acid encoding feline CD86 ligand or feline
XX soluble CD80 ligand is designated PSI-2#19-2/011298 (ATCC 209821).
XX The coexpression of CD86 with the costimulatory molecules CD28 (see
XX AAY32279) and a tumour antigen or an antigen from a pathogenic
XX organism has the ability to activate or enhance activation of
XX T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has
XX the ability to regulate activation of T-lymphocytes. The invention
XX provides isolated nucleic acids encoding feline CD86 ligand,
XX feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
XX (CD152) receptor, as well as vectors comprising the nucleic acids,
XX and polypeptides encoded by the nucleic acids. It also provides
XX vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
XX further comprising immunogens derived from pathogens, especially
XX feline immunodeficiency virus (FIV), feline leukaemia virus,
XX feline infectious peritonitis virus, feline panleukopenia virus,

```



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AC AA227931;
XX
XX 20-DEC-1999 (first entry)
XX
XX
DE Feline B7-2 protein coding sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX P-PSDB; AA41079.
XX
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1; Page 123-124; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other:
XX
Query Match 63.3%; Score 227.2; DB 20; Length 996;
Best Local Similarity 94.8%; Pred. No. 2.8e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
XX 1 ATACAAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60.
XX |||||||
DB 484 ATACAAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 543
XX
XX 61 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGACAGAACTGTACAACGTT 120
XX |||||||
DB 544 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGAGACAACTGTACAACGTT 603
XX
XX 121 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAATGTGAGCGCTTTGTGCCCTG 180
XX |||||||
DB 604 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAATGTGAGCGCTTTGTGCCCTG 663
XX
XX 181 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 240
XX |||||||
DB 664 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 723
XX
XX 241 GAGAGAAA 248
XX |||||
DB 724 GATAAAGA 731
XX
RESULT 40
AA227932/c
ID AA227932 standard; DNA; 996 BP.
```

```
XX
XX AA227932;
XX
XX 20-DEC-1999 (first entry)
XX
XX
XX Complementary strand of feline B7-2 coding sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
XX
XX WO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI; 1999-571822/48.
XX
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1; Page 124-125; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other:
XX
Query Match 63.3%; Score 227.2; DB 20; Length 996;
Best Local Similarity 94.8%; Pred. No. 2.8e-57;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
XX
XX 1 ATACAAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60
XX |||||||
DB 513 ATACAAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 454
XX
XX 61 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGACAGAACTGTACAACGTT 120
XX |||||||
DB 453 ACTAAGTATGATCTGCTATGAGAAATCTCAAAATATATGAGACAACTGTACAACGTT 394
XX
XX 121 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAATGTGAGCGCTTTGTGCCCTG 180
XX |||||||
DB 393 TCTATCAGCTTCGCTTTTTCAGTCCCTGAAGACACAATGTGAGCGCTTTGTGCCCTG 334
XX
XX 181 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 240
XX |||||||
DB 333 AAACGTGAGACACTGAGAGATGCTGCTCCCTACCTTTCAATATAGAAACCATAAAGG 274
XX
XX 241 GAGAGAAA 248
XX |||||
DB 273 GATAAAGA 266
XX
RESULT 11
AA234838
ID AA234838 standard; cDNA; 1080 BP.
```

DT	20-DEC-1999	(first entry)
DE	Feline B7-2 protein (larger fragment) encoding DNA.	
DN		
DR		
DS		
DX		
EY		
FM	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;	
GN	allergic reaction; infectious disease; tumor development; feline;	
HM	graft rejection; inflammation; arthritis; atopic dermatitis; ss.	
IN		
KX		
OS	Felis catus.	
PB		
PN	W099947558-A2.	
PD	23-SEP-1999.	
PE	19-MAR-1999; 99WO-US06187.	
PF		
PI	19-MAR-1998; 98US-0078765.	
PR	17-APR-1998; 98US-0062597.	
PS	(HESK-) HESKA CORP.	
PT	Sim G., Yang S., Sellins KS;	
XX	WPI; 1999-571832/48.	
XX	P-PDB; AAY41080.	
XX	New isolated B7 and CTLA4 nucleic acids; used to develop products for treating, e.g. autoimmune and atopic diseases -	
XX	Claim 1; Page 125-126; 148pp; English.	
XX	The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritis and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.	
XX	Sequence 509 BP; 170 A; 109 C; 106 G; 124 T; 0 other;	
SQ		
Query Match	63.3%; Score 227.2; DB: 20; Length 509;	
Best Local Similarity	94.8%; Pred. No. 2.2e-57;	
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0		
QY	1 ATACAGGTTATCTGTGCATGAAGAATCTCAAAATATGTGACAGAACTGTACAACGT 60	
DB	1 ATACAGGTTATCTGTGCATGAAGAATCTCAAAATATGTGACAGAACTGTACAACGT 60	
OY	ACTAGTAGTATCTGTGCATGAAGAATCTCAAAATATGTGACAGAACTGTACAACGT 120	
DB	61 ACTAGTAGTATCTGTGCATGAAGAATCTCAAAATATGTGACAGAACTGTACAACGT 120	
OY	121 TCATCAGCTTGCCCTTTTCAGTCCCTGAAGCACAAATGTGAGCGCTTTTGTGCCCTG 180	
DB	121 TCATCAGCTTGCCCTTTTCAGTCCCTGAAGCACAAATGTGAGCGCTTTTGTGCCCTG 180	
OY	181 AAACGTGAGACACTGGAGATGCGTCCCTCCCAACTTTCATTATAGAACCATCAAAAGG 240	
DB	181 AAACGTGAGACACTGGAGATGCGTCCCTCCCAACTTTCATTATAGAGACACAACTTAAG 240	
OY	241 GAGAGAAA 248	
DB	241 GATTAAGA 248	

RESULT: 8
AAZ27934/c
ID AAZ27934 standard; DNA; 509 BP.
XX

AC	AAZ27934.
XX	
DT	20-DEC-1999 (first entry)
XX	
DE	Feline B7-2 gene (larger fragment) complementary DNA sequence.
XX	
KW	B7; CTIA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM	allergic reaction; infectious disease; tumor development; feline;
KM	graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX	
OS	Felis catus.
XX	
FN	M09947558-A2.
XX	
PD	23-SEP-1999.
XX	
PF	19-MAR-1999; 99MO-US06187.
XX	
PR	19-MAR-1998; 98US-0078765-
PR	17-APR-1998; 98US-0062597.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Slim G., Yang S., Sellins KS;
DR	WPI; 1999-571822/48.
XX	
PT	New isolated B7 and CTIA4 nucleic acids, used to develop products for
XX	treating, e.g. autoimmune and atopic diseases
PS	Claim 1; Page 127; 148pp; English.
XX	
CC	The invention provides B7 and CTIA4 (T cell costimulatory proteins)
CC	encoding nucleic acid molecules from dogs and cats. The proteins can be
CC	expressed by standard recombinant methodology. The nucleic acid molecules
CC	and the encoded proteins can be used for preventing or treating diseases,
CC	e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC	development, graft rejection, inflammation, arthritic and atopic diseases
CC	such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC	cats, cattle, sheep or pets. The products can also be used for detection,
CC	diagnosis and drug screening.
XX	
SQ	Sequence 509 BP; 124 A; 106 C; 109 G; 170 T; 0 other;
XX	
Query Match	63.3%; Score 227.2; DB 20; Length 509;
Best Local Similarity	94.8%; Pred. No. 2,2e-57;
Matches 235; Conservative	0; Mismatches 13; Indels 0; Gaps 0.
OY	I ATACAAGGTTACCAGAACCTAAGAGATGTATTTTCAGCTAAACTGAGAATTCAACT 60
DB	509 ATACAAGGTTACCAGAACCTAAGAGATGTATTTTCAGCTAAACTGAGAATTCAACT 450
OY	61 ACTAAGTAGTGATCTCGCATGAAGAAATCTCAAATTAATGGACAGAACTGTACAACGTT 120
DB	449 ACTAAGTAGTAGTACTGTCTCAGAAAGAAATCTCAAATTAATGGACAGAACTGTACAACGTT 390
OY	121 TCATACAGCTTGCCCTTTTCAGTCCCTCGAAGCACACAATGTGAGCGCTTTTGTGCCCTG 180
DB	389 TCATACAGCTTGCCCTTTTCAGTCCCTCGAAGCACACAATGTGAGCGCTTTTGTGCCCTG 330
OY	181 AAATCGAGACACTGGAGATGCCTGCTCCACCTTCATATAGAAACCATCAAAAGG 240
DB	329 AAATCGAGACACTGGAGATGCTCTCTCTCCACTTCATATATAGATGCACAACTAAG 270
OY	241 GAGAGAAA 248
DB	269 GATAAAGA 262
RESULT 9	
ID	AAZ27931
XX	AAZ27931 standard; DNA; 996 BP.

xx	Canis familiaris.
xx	
FN	W09947558-A2.
xx	
PD	23-SEP-1999.
xx	
PF	19-MAR-1999; 99WO-US06187.
xx	
PR	19-MAR-1998; 98US-0078765.
PR	17-APR-1998; 98US-0062597.
xx	(HESK-) HESKA CORP.
PA	
XX	
PI	Sim G., Yang S., Sellins KS;
DR	MPL; 1999-571822/48.
P-P	P-SDB; AAY41078.
xx	
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases -
xx	
PS	Claim 1; Page 109-111; 148pp; English.
xx	
CC	The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritis and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.
CC	
xx	
SQ	Sequence 1795 BP; 592 A; 366 C; 347 G; 490 T; 0 other;
	Query Match 75.5%; Score 271; DB 20; Length 1795;
	Best Local Similarity 86.6%; Pred. No. 3.9e-70;
	Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1.
OY	1 ATACAAGGTTACCCAACAACTAAGAGATGTATTTCAGTAACACTGAGAATTCACT 60 Db 487 ATACAAGGTTACCCAACAAACCAGAGATGTATTTTTTGCTMAAACCGGAATTCACT 546
OY	61 ACTAAGTAGTATCTGTCTCATGAAGAAATCTCAAATAATATGTGACAGAACTGTACACGTT 120 Db 547 ACTAAGTAGTATCTGTCTCATGAAGAAATCTCAAATAATATGTGACAGAACTGTACACGTT 606
OY	121 TCATCAGCTGGCTTTTCAGTCCCTGAGACACATGTGAGCGCTTTTGTGCCCTG 180 Db 607 TCATCAGCTGTGCCTTCCTTCAGTCCCTGAGACACATGTGAGCACATCTTCTGTGTCCTG 666
OY	181 AAATCGAGACACTGSAGATGCTGCTCTTCCTTACCTTTCAATATAGAACCATTCAAAAGS 240 Db 667 CAATCTTAGCAAT---GAAGCTTCCTCCCTTACCTTATTAATATAGAACAACAAAGTG 723
OY	241 GAGAGAAAAGAGACAACAAACGAAAGAGTACCATCCACGATACCTGAGAGACT 300 Db 724 GAGAGAAAAGAAAGTGAGACAGCAAGGAAGAGTACCATCCATGAAAGGAAAGTCT 783
OY	301 GATGAGCCCGACGTGTATTAACATTTTGAAGACAGCTTAGAGCGCAAAAGTACTACACA 359 Db 784 GATGAGCCCGACGTGTGTATTAACATTTTGAAGACAGCTTAGAGCGCAACAGTACTACACA 842
RESULT 6	
ID	AAZ27922/C
xx	AAZ27922 standard; DNA; 1795 BP.
AC	AAZ27922;
xx	
TF	20-DEC-1999 (first entry)
xx	
DE	Canine B7-2S gene complementary DNA sequence.

B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease; allergic reaction; infectious diseases; tumor development; canine; graft rejection; inflammation; arthritis; atopic dermatitis; ss.
Canis familiaris.
XX MO9947558-A2.
PX 23-SEP-1999.
PF 19-MAR-1999; 99WO-US06187.
PR 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
PA (HESK-) HESKA CORP.
PI Slim G, Yang S, Sellins KS;
DR WPI: 1999-571822/48.
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for treating, e.g. autoimmune and atopic diseases
PS Claim 1; Page 112-114; 148pp; English.
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.
SQ Sequence 1795 BP; 490 A; 347 C; 366 G; 592 T; 0 other;
Query Match 75.5%; Score 271; DB 20; Length 1795; Best Local Similarity 86.6%; Pred. No. 3,9e-70;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1
OY 1 ATCAAGGTTACCCAGACCTTAAGAATGTATTTCAGCTAAACACTGAGAATTCACCT 60 Db 1309 ATACAAGGTTACCCAGACCTTAAGAATGTATTTCAGCTAAACACTGAGAATTCACAGT 1250
OY 61 ACTAAGATATATCTGCATGAGAAGAAATCTCAAATTAATGTGACAGAAGTGTAACAAGTT 120 Db 1249 ACTAAGATATATCTGCATGAGAAGAAATCTCAAATTAATGTGACAGAAGTGTAACAAGTT 1190
OY 121 TCATACGCTTGGCCTTTTTCAGTCCCTGAACACAAATGTGAGCGTCTTTTGCCCTG 180 Db 1189 TCATACGCTTGGCCTTTTTCAGTCCCTGAACACAAATGTGAGCATCTCTGTGCTG 1130
OY 181 AAATCGAGACACTGAGATGCTGCTGCCACCTTCATATATGAAGAACCATAAAGS 240 Db 1129 CAATTTAGTCAAT---GAAAGTCCCTCCACTCTTAAATATGACAAACCAAAAGTS 1073
OY 241 GAGGAAAAAGAGACAAACAGCACAAAGAGATGCATATCCATCCACGTCATCTGAGAGTCT 300 Db 1072 GAGGAAAAAGAGAGTAGGACAAAGAAAGATGATCCATGGAAGCGAAAAGTCT 1013
OY 301 GATCAACCCCAAGTGATATTAACATTTTGAAGACAGGCTTAGCGCGCAAAAGTACTACACA 359 Db 1012 GATCAACCCCAAGTGATATTAACATTTTGAAGACAGGCTTAGCGCGCAACAGTACTACACA 954
RESULT 7 AAZ27933 ID AAZ27933 standard; DNA: 509 BP. XX AAZ27933; NC

PR 17-APR-1998: 98US-0062597.
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
DR P-PSDB: AAY41078.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX
PS Claim 1, Page 114, 148pp: English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP: 278 A; 181 C; 167 G; 214 T; 0 other;
Query Match 75.5%; Score 271; DB 20; Length 840;
Best Local Similarity 86.6%; Pred. No. 3e-70;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
OY 1 ATACAGGTTACCCAGAACCTAGAGATGTATTTTCAGCTAAGACAGATTTCACT 60
DB 481 ATACAGGTTACCCAGAACCCAGAGATGTATTTTGTGTAACCGAGATTTCACT 540
OY 61 ACTAAGTATGATGTCTCATGAAGAATCTCAAAATATGTGACAGAACTGTACAGCTT 120
DB 541 ACTAAGTATGATGTCTCATGAAGAATCTCAAAATATGTGACAGAACTGTACAGCTT 600
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
DB 601 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 660
OY 181 AAACGTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATATAGAAACCATCAAGG 240
DB 661 CAACCTGAGTCAT--GAAGCTTCCCTCCCTACCTTATATATAGAAACCATCAAGG 717
OY 241 GAGAGAAAAGAGACAAACAGACCAAGAGATACATCCAGCTACGAGAGATCT 300
DB 718 GAGAGAAAAGAGAGACAGACCAAGAGATACGATACGAGAGAGAGATCT 777
OY 301 GATGAAGCCAGGTATTAACATTTTGAAGACAGCCTCAGCGACAAAGTACTACACA 359
DB 778 GATGAAGCCAGGTATTAACATTTTGAAGACAGCCTCAGCGACAAAGTACTACACA 836
RESULT 4
AAZ27924/c
ID AAZ27924 standard; DNA: 840 BP.
XX
XX AAZ27924;
AC
XX
XX 20-DEC-1999 (first entry)
DT
XX
XX Complementary strand of canine B7-2S coding sequence.
DE
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
OS
XX
XX W09947558-A2.
PN

PD 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
DR
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX
PS Claim 1, Page 115, 148pp: English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP: 214 A; 167 C; 181 G; 278 T; 0 other;
Query Match 75.5%; Score 271; DB 20; Length 840;
Best Local Similarity 86.6%; Pred. No. 3e-70;
Matches 311; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
OY 1 ATCAAGGTTACCCAGAACCTAGAGATGTATTTTCAGCTAAGACAGATTTCACT 60
DB 360 ATCAAGGTTACCCAGAACCCAGAGATGTATTTTGTGTAACCGAGATTTCACT 301
OY 61 ACTAAGTATGATGTCTCATGAAGAATCTCAAAATATGTGACAGAACTGTACAGCTT 120
DB 300 ACTAAGTATGATGTCTCATGAAGAATCTCAAAATATGTGACAGAACTGTACAGCTT 241
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 180
DB 240 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 181
OY 240 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 181
DB 240 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGCTTTTGTGCCCTG 181
OY 181 AAACGTGAGACACTGAGATGCTGCTCTCCCTACCTTTCAATATATAGAAACCATCAAGG 240
DB 180 CAACCTGAGTCAT--GAAGCTTCCCTCCCTACCTTATATATAGAAACCATCAAGG 124
OY 241 GAGAGAAAAGAGACAAACAGACCAAGAGATACATCCAGCTACGAGAGATCT 300
DB 123 GAGAGAAAAGAGAGACAGACCAAGAGATACGATACGAGAGAGAGATCT 64
OY 301 GATGAAGCCAGGTATTAACATTTTGAAGACAGCCTCAGCGACAAAGTACTACACA 359
DB 63 GATGAAGCCAGGTATTAACATTTTGAAGACAGCCTCAGCGACCAAGTACTACACA 5
RESULT 5
AAZ27921
ID AAZ27921 standard; DNA: 1795 BP.
XX
XX AAZ27921;
AC
XX
XX 20-DEC-1999 (first entry)
DT
XX
XX Canine B7-2S protein encoding DNA.
DE
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1, Page 127-128; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 359 BP; 128 A; 79 C; 69 G; 83 T; 0 other:

Query Match 100.0%; Score 359; DB 20; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAACACTGGAATTCACCT 60
Db 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAACACTGGAATTCACCT 60

QY 61 ACTAAGTATGATCTGCTCATGAGAAATCTCAAAATATGTGACAGAACTGACAGCTT 120
Db 61 ACTAAGTATGATCTGCTCATGAGAAATCTCAAAATATGTGACAGAACTGACAGCTT 120

QY 121 TCTATGAGCTTGCTTTTCACTCCCTGAGACACAAATGTGAGCGCTTTTGCCCTG 180
Db 121 TCTATGAGCTTGCTTTTCACTCCCTGAGACACAAATGTGAGCGCTTTTGCCCTG 180

QY 181 AAACCTGAGACACTGAGATGCTGCTGCCCTACCTTCATATGAGAAACATCAAAAG 240
Db 181 AAACCTGAGACACTGAGATGCTGCTGCCCTACCTTCATATGAGAAACATCAAAAG 240

QY 241 GAGAGAAAAGAGACAAACAGACAAAGAGATGATGATGATGATGATGATGATGAT 300
Db 241 GAGAGAAAAGAGACAAACAGACAAAGAGATGATGATGATGATGATGATGATGAT 300

QY 301 GATGAGCCCAAGTGTATTAACATTTTGAAGACAGCTCAGGCGAAGAAAGTACTACCA 359
Db 301 GATGAGCCCAAGTGTATTAACATTTTGAAGACAGCTCAGGCGAAGAAAGTACTACCA 359

RESULT 2
AA27936/c
ID AA27936 standard; DNA; 359 BP.

XX AA27936;
XX
DT 20-DEC-1999 (first entry)

XX Feline B7-2 gene (smaller fragment) complementary DNA sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Felis catus.

XX WO9947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Sellins KS;

DR WPI: 1999-571822/48.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases

PS Claim 1, Page 129; 148bp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 359 BP; 83 A; 69 C; 79 G; 128 T; 0 other:

Query Match 100.0%; Score 359; DB 20; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-96;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAACACTGGAATTCACCT 60
Db 359 ATACAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAACACTGGAATTCACCT 300

QY 61 ACTAAGTATGATCTGCTCATGAGAAATCTCAAAATATGTGACAGAACTGACAGCTT 120
Db 299 ACTAAGTATGATCTGCTCATGAGAAATCTCAAAATATGTGACAGAACTGACAGCTT 240

QY 121 TCTATGAGCTTGCTTTTCACTCCCTGAGACACAAATGTGAGCGCTTTTGCCCTG 180
Db 121 TCTATGAGCTTGCTTTTCACTCCCTGAGACACAAATGTGAGCGCTTTTGCCCTG 180

QY 239 TCTATGAGCTTGCTTTTCACTCCCTGAGACACAAATGTGAGCGCTTTTGCCCTG 180
Db 239 TCTATGAGCTTGCTTTTCACTCCCTGAGACACAAATGTGAGCGCTTTTGCCCTG 180

QY 181 AAACCTGAGACACTGAGATGCTGCTGCCCTACCTTCATATGAGAAACATCAAAAG 240
Db 179 AAACCTGAGACACTGAGATGCTGCTGCCCTACCTTCATATGAGAAACATCAAAAG 120

QY 241 GAGAGAAAAGAGACAAACAGACAAAGAGATGATGATGATGATGATGATGATGAT 300
Db 119 GAGAGAAAAGAGACAAACAGACAAAGAGATGATGATGATGATGATGATGATGAT 60

QY 301 GATGAGCCCAAGTGTATTAACATTTTGAAGACAGCTCAGGCGAAGAAAGTACTACCA 359
Db 59 GATGAGCCCAAGTGTATTAACATTTTGAAGACAGCTCAGGCGAAGAAAGTACTACCA 1

RESULT 3
AA27923
ID AA27923 standard; DNA; 840 BP.

XX AA27923;
XX
DT 20-DEC-1999 (first entry)

XX Canine B7-2S protein coding sequence.

XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; canine;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Canis familiaris.

XX WO9947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 54.2731 Seconds
(without alignments)

11356.866 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggtaccagacc.....gacgacaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.GeneSeq_032802.*
1: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT.*
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6: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1989.DAT.*
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12: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	359	20	AAZ27935
c	359	100.0	359	20	AAZ27936
3	271	75.5	840	20	AAZ27923
c	271	75.5	840	20	AAZ27924
5	271	75.5	1795	20	AAZ27921
c	271	75.5	1795	20	AAZ27922
7	227.2	63.3	509	20	AAZ27933
c	227.2	63.3	509	20	AAZ27934
9	227.2	63.3	996	20	AAZ27931

c	10	227.2	63.3	996	20	AAZ27932	Complementary strA
c	11	227.2	63.3	1080	21	AAZ34838	Feline CD86 (B7-2)
c	12	227.2	63.3	1080	21	AAZ34785	Cat CD86 (B7-2) cd
c	13	227.2	63.3	2830	20	AAZ27929	Feline B7-2 protei
c	14	227.2	63.3	2830	20	AAZ27935	Feline B7-2 gene c
c	15	169.4	47.2	987	20	AAZ27915	Canine B7-2 protei
c	16	169.4	47.2	987	20	AAZ27916	Complementary strA
c	17	169.4	47.2	1897	20	AAZ27913	Canine B7-2 protei
c	18	169.4	47.2	1897	20	AAZ27914	Canine B7-2 gene c
c	19	124.6	34.7	1050	21	AAA49661	Pig costimulatory
c	20	110	30.6	306	18	AAZ49198	Human B lymphocyte
c	21	110	30.6	306	18	AAZ49198	Human B7-2 constan
c	22	110	30.6	738	20	AAZ80293	Human B7-2 extrac
c	23	110	30.6	738	20	AAZ80293	Nucleotide sequenc
c	24	110	30.6	764	18	AAZ2939	Chimeric human/por
c	25	110	30.6	831	19	AAV0320	DNA encoding CD86
c	26	110	30.6	972	20	AAV63208	B7-2 cDNA. Homo s
c	27	110	30.6	972	24	AAZ25510	Human co-stimulato
c	28	110	30.6	1120	16	AAZ81351	Human B lymphocyte
c	29	110	30.6	1120	18	AAZ49181	Human B lymphocyte
c	30	110	30.6	1120	20	AAV55764	Human B7-2 antigen
c	31	110	30.6	1120	21	AAZ4918	Human B lymphocyte
c	32	110	30.6	1424	21	AAZ29321	Human B7-2 cDNA.
c	33	110	30.6	1428	16	AAZ05873	B70 type B antigen
c	34	110	30.6	2205	22	AAH72616	Human cervical can
c	35	78	21.7	210	16	AAZ01038	Borrelia burgdorfe
c	36	77.2	21.5	1151	20	AAV55785	Human B7-2 antigen
c	37	77.2	21.5	1163	16	AAZ81366	Mouse B lymphocyte
c	38	77.2	21.5	1163	18	AAZ49182	Mouse B lymphocyte
c	39	77.2	21.5	1163	21	AAZ84050	Mouse B lymphocyte
c	40	77.2	21.5	1261	16	AAZ01046	Rat CD86 coding se
c	41	66	18.4	942	19	AAZ9926	Borrelia burgdorfe
c	42	36.8	10.3	1030	20	AAZ20338	Drosophila melanog
c	43	36	10.0	1309	20	AAZ0323	Human immune syste
c	44	35.4	9.9	15306	23	ABL15764	
c	45	34.6	9.6	11726	24	ABL34063	

ALIGNMENTS

AAZ27935	standard: DNA; 359 BP.
AAZ27935	
AAZ27935	
20-DEC-1999	(first entry)
Feline B7-2 protein (smaller fragment) encoding DNA.	
B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;	
allergic reaction; infectious disease; tumor development; feline;	
graft rejection; inflammation; arthritis; atopic dermatitis; ss.	
Felis catus.	
WO9947558-A2.	
23-SEP-1999.	
19-MAR-1999;	99WO-US06187.
19-MAR-1998;	98US-0078765.
17-APR-1998;	98US-0062597.
(HESK-) HESKA CORP.	
Sim G, Yang S, Sellins KS;	
WPI: 1999-571822/48.	
P-PDB; AA141081.	

LOCUS	BE823527	553 bp	mRNA	linear	EST 24-MAY-2001			
DEFINITION	Gm-r1070 glycine max CDNA clone Gm-r1070-8311 3', mRNA sequence.							
ACCESSION	BE823527							
VERSION	BE823527.1	GI:10255712						
KEYWORDS	EST.							
SOURCE	soybean.							
ORGANISM	Glycine max							
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae; Glycine.							
REFERENCE	1. (bases 1 to 553) Shoemaker R., Retzel, E., Khanna A., Coryell, V., Vodkin, L., Kelm, P., A functional genomics Program for Soybean (NSF 9872563) unpublished (1995)							
AUTHORS	Other_ESTs: AW508748 corresponding to Gm-r1030-965 (5')							
TITLE	A functional genomics Program for Soybean (NSF 9872563)							
JOURNAL	Other_ESTs: AW508748 corresponding to Gm-r1030-965 (5')							
COMMENT								

FEATURES

Source

BASE COUNT
ORIGIN

185 a 116 c 101 g 130 t 21 others

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="Gm-r1070-8311"
/clone_lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Reitzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, <http://www.cbc.umn.edu/researchProjects/Soybean/Index.html>. Reracking was performed by Genome Systems, St. Louis, <http://www.genomesystems.com>, and 3' sequencing by the Beck Center for Comparative and Functional Genomics, University of Illinois, <http://www.life.uiuc.edu/biotech/beck.html>. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

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Query Match      10.8%; Score 38.6; DB 10; Length 553;
Best Local Similarity 51.4%; Pzed.No. 37;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0.
OY 145-CCCTAAGCACACATGTGAGCGCTCTTTTTCGCCGAAACGTGAGACACTGAGCATCCTG 204
      || || || || || || || || || || || || || || || || || || || || ||

```

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Db 166 CCGAGGAGGAGAAATGTGATGTGTTAGGGCCCTGACCAACAAAATACTATGGTAGTG 225
QY 205 CTCTCCCTACCTTTCAATATATGAAACCATCAAAAGGAGAGAAAGACCAACACAGACC 264
      |||||      |||
Db 226 TCTCTCCCTCTCTCTCCATCAAAACCTTTTGGCAAAAGGATATGAGATGACCAAGCCCAA 285
      |||||      |||
QY 265 AACGAAAGAGTACCATACCACTAGCTACGTGAGACGATCTGATGAAGCCCACTGAT 317
      ||| |||| ||| |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 AACTGAAAGAAACACCACCAAGTAGAGCGGCTCCACTGTGTGATGACACTGTAT 338
      ||| |||| ||| |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: October 20, 2002, 04:30:18
Job time : 435.863 secs

Search completed: October 20, 2002, 04:30:18
Job time : 435.863 secs

source

1. 486
/organism="Sus scrofa"
/strain="crossbred"
/db_xref="taxon:9823"
/clone_lib="Porcine lymph node cDNA library, Cot 5"
/tissue_type="lymph node"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/note="Vector: pBSK. Site_1: Eco RI. Site_2: XhoI. Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGACAGC'."

BASE COUNT 144 a 98 c 75 g 150 t 19 others
ORIGIN

Query Match 15.5%; Score 55.8; DB 10; Length 486;
Best Local Similarity 73.2%; Pred. No. 0.0035;
Matches 101; Conservative 0; Mismatches 28; Indels 9; Gaps 2;

OY 225 AGAACCATCAAAAGAGAGAAAGAGCAACAGCAGCAAGAGAGTACCATACCA 284
|||||
DB 10 AGAACCATCAAAAGAGAGAGCAACAGCAGCAAGAGAGTACCATACCA 284
|||||
OY 285 CGTACTGAGAGATCTGATGAAGCCCACTGTA---TTTACATTTTGAAGACAGCTCAGG 341
|||||
DB 64 AGTCATGAAGAGATCTGATGAAGCCCACTGTAATATTTTAAAGACAGCTCAGG 123
|||||
OY 342 CGACAAAGTACTACACA 359
|||||
DB 124 TGACAAAGTACTACAGA 141

RESULT 11
AI632116/c 391 bp mRNA linear EST 14-DEC-1999
LOCUS ts85b01.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2238025 3
DEFINITION similar to SW:CD6_HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN
CD66 PRECURSOR ; mRNA sequence.
AI632116
ACCESSION AI632116.1 GI:4683446
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 391)
NCI-CGAP <http://www.nci.nlm.nih.gov/ncicgap>.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert length: 461 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES

1. 391
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2238025"

/clone_lib="NCI CGAP GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI. Plasmid DNA
from the normalized library NCI-CGAP-GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldi."

BASE COUNT 115 a 68 c 92 g 116 t
ORIGIN

Query Match 11.8%; Score 42.2; DB 9; Length 391;
Best Local Similarity 79.7%; Pred. No. 5.2;
Matches 63; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

OY 282 CCACGTACTGAGAGATCTGATGAAGCCCACTG---TATTACATTTTGAACAGACCTTC 338
|||||
DB 388 CCATATACCTGAAGATCTGATGAAGCCCACTGTTTAAAGTTGGAAGACATCTTC 329
|||||
OY 339 AGCGACAAAGTACTACA 357
|||||
DB 328 ATCGACAAAGTACTACA 310

RESULT 12
BG252809 858 bp mRNA linear EST 13-FEB-2001
LOCUS BG252809 602365378P1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4473739 5'
DEFINITION mRNA sequence.
ACCESSION BG252809
VERSION BG252809.1 GI:12762625
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 858)
NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNM10296 row: k column: 20
High quality sequence stop: 283.

FEATURES

1. 858
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4473739"
/clone_lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; Oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

BASE COUNT

500 a 155 c 144 g 59 t

Query Match 11.4%; Score 40.8; DB 10; Length 858;
Best Local Similarity 56.8%; Pred. No. 12;

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc

implant-associated infection using 1000 *cid* and 1000 *scaphylococcus aureus* in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'.

FEATURES

Location/Qualifiers

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VERSION      BF064222.1   GI:10823132
KEYWORDS
SOURCE       EST
ORGANISM     human.
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS      1 (bases 1 to 543)
              NCI-CCAG http://www.ncbi.nlm.nih.gov/ccagap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: ccgaps@mail.nih.gov
              This clone is available royalty-free through LNLN ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Seq primer: -40UP from Gldco
              High quality sequence stop: 496.
FEATURES
SOURCE
1..543
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:3380507"
    /clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"
    /lab_host="DH10B"
    /note="Organ: pooled. Vector: pRTT3D-Pac (Pharmacia) with
    a modified polylinker. Site_1: Not I; Site_2: Eco RI;
    Equal amounts of plasmid DNA from five normalized
    libraries were mixed, and ss circles were made in vitro.
    Following HAP purification, this DNA was used as tracer in
    PCR-amplified cDNAs from pools of 5,000 clones made from
    the same 5 libraries. The pools consisted of the following
    libraries and cloneids: Soares NBHP pool 1 :
    309384-310919, 333208-325895 Soares NBHP pool 1 :
    145032-147335, 147720-148103, 146871-149255, 15002 -
    150407, 151176-152327 Soares NB2HF8-9W pool 1 :
    758280-760583, 772104-774407 Soares NBdPA pool 1 :
    304776-306311, 320136-322823, 326280-326663 Soares NBHOT
    pool 1 : 723720-726407, 739080-740999 Subtraction by Bento
    Soares and M. Fatima Bonaldo."
BASE COUNT   151 a      104 c      112 g      175 t      1 others
ORIGIN
Query Match          21.3% Score 76.4; DB 10; Length 543;
Best Local Similarity 70.5%; Pred. No. 5.2e-08;
Matches 117; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
CY 195 GGAGATGCTGCTCTCCTCACTTCATATPATAAACCATCAANAAGGGAGAAAAGAGAG 254
         ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 466 GAACAAACGCCCTCCGACTTTATTAAATGTGAACAACCAACATGTGAGGGAGAAGAG 407
CY 255 CAACAGACCAAGAGAAGTAGTACCTATACAGCTGTAAGAGATCTGATAACCCAGTG 314
         ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 406 TGAAACAGACCAAGAAAAGAAAAATCATATPACTGTGAAGATCTGATAAACCCAGG 347
CY 315 ---TATTAACTTTGAAGACAGCCGTCAGGGAGCAAAAGTACTCTCA 357
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DB 346 TGTTTTAAAGTTCCAGAGCACTCTCAATGCAGCAAAAGTATACA 301

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RESULT 7
A1750143/c A1750143 480 bp mRNA linear EST 22-JUN-1999
DEFINITION at27n10.x1 Barsstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:235687 3' similar to SW:CD86, HUMAN P42081 T LYMPHOCTYME
ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.
ACCESSION A1750143
VERSION A1750143.1 GI:5128407
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Cranialta; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

[illegible]

Db 328 TGTTTTAAAGTTCGAGACATCTTCATGCGACAAAAGTGATACA 373

RESULT 4
 A1093604/c 570 bp mRNA linear EST 10-NOV-1998
 LOCUS ou82b09.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:1634297.3' similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE
 ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.

ACCESSION A1093604
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 570)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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FEATURES
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 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with
 a modified polylinker; Site:1: Not I; Site:2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and clones: Soares NBHSP pool 1:
 309384-310919, 323208-325895 Soares NB2HP pool 1:
 145032-14735, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares NBHFP-9W pool 1:
 758280-760583, 772104-774407 Soares NBHFA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NBHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 107 c 134 g 179 t

ORIGIN

Query Match 21.5%; Score 77.2; DB 9; Length 570;
 Best Local Similarity 73.4%; Pred. No. 3.4e-08;
 Matches 113; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Db 207 CTCCTACCTTCATATAGAACATCAAGGAGAGAAAGAGCAAGACACCA 266
 452 CTGGCACTCTATATAAGTGACACACATGAGAGAGAGTGACAGACCA 393

QY 267 CGAAGAGTACCATACCATGAGAGATCTGATGAGAGCCAGTG--TATTACAT 323
 392 GAAAGAGAAAAAATCCATATACCTGAAAGATCTGATGAAACCCAGCGTCTTTAAAG 333

Db 324 TTTGAAGAGAGCGCTCAGGCGACAAAAGTACTACA 357
 332 TTTCGAGACATCTTCATGCGACAAAAGTGATACA 299

RESULT 5
 AA946810/c

LOCUS AA946810 504 bp mRNA linear EST 23-JUL-1998
 DEFINITION ou43c01.s1 NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1589088.3'
 similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN
 CD86 PRECURSOR ; mRNA sequence.

ACCESSION AA946810
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 1 (bases 1 to 504)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bbrp/image/image.html
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 High quality sequence stop: 457.

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 strand cDNA was primed with a Not I - oligo(dt) primer [5'
 AACATGAGAAATTCGCGCGCCGCAATATTTTCTTTTCTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT3D vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 136 a 94 c 109 g 165 t

ORIGIN

Query Match 21.3%; Score 76.4; DB 9; Length 504;
 Best Local Similarity 70.5%; Pred. No. 5.2e-08;
 Matches 117; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

Db 195 GGAAGATGCTGCTCTCCTTCAATATAGAACATCAAAAGGAGAGAAAGAG 254
 472 GAAGAGCGGCTCGACACTTATATATGGAACCAACCAATGAGGAGAGAG 413

QY 255 CAAGAGACCAAGAGAGTACATACACAGTACAGATCTGATGAGAGCCAGTG 314
 412 TGACAGACCAAGAGAGAAAGAAATTCATATACCTGAAAGATCTGATGAAACCCAGCG 353

Db 315 --TATTACATTTTGAAGACAGCTCAGGCGACAAAAGTACTACA 357
 352 TGTTTTAAAGTTTCGAAAGACATCTTCATGCGACAAAAGTGATACA 307

RESULT 6
 BF064222/c

LOCUS BF064222 543 bp mRNA linear EST 16-OCT-2000
 DEFINITION 7j57b02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:3390507.3' similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE
 ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.

ACCESSION BF064222

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 427.863 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggtaccacgaac.....ggcagacaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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2: em_esthum:*
3: em_estlin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	104.8	29.2	512	9	AA056905 EST224F.P
c 2	84	23.4	753	10	BI906246 603063172
c 3	78	21.7	496	9	AW516826 xq04h01.x
c 4	77.2	21.5	570	9	AI093604 ou82b09.s
c 5	76.4	21.3	504	9	AA946810
c 6	76.4	21.3	543	10	BF064222
c 7	72.4	20.2	480	9	AT750143
c 8	64.8	18.1	347	10	BG001664 RC4-GN006
c 9	57.8	16.1	1002	10	BF137460 601780644
c 10	55.8	15.5	486	10	BI132458 AR031A11L
c 11	42.2	11.8	391	9	AT632116 ts85b01.x
c 12	40.8	11.4	858	10	BG252809 602365378
c 13	40.4	11.3	378	9	AA973397
c 14	39	10.9	538	12	TA254E04P
c 15	38.6	10.8	583	10	BE823527 GM700021A
c 16	38.2	10.6	654	12	AZ233626 RPCI-23-9
c 17	38	10.6	565	9	BE118052 UI-R-B51-

18	37.8	10.5	692	9	AV723257	AV723257
19	37.4	10.4	619	12	FR0004538	Z88321 F.rubripes
c 20	37.2	10.4	690	12	A2220823	A2220823 Sheared D
c 21	37	10.3	386	10	BE921966	BE921966 EST425755
c 22	37	10.3	484	10	BG511725	BG511725 sad42c05.
c 23	37	10.3	496	10	BG510033	BG510033 sad26g11.
c 24	37	10.3	512	12	AQ342188	AQ342188 RPCI11-12
c 25	37	10.3	679	10	BM406580	BM406580 EST580907
c 26	36.6	10.2	275	9	BA426183	BA426183
c 27	36.6	10.2	760	10	BE262554	BE262554 601154211
c 28	36.4	10.1	294	12	AZ510008	AZ510008 IM0354P10
c 29	36.4	10.1	1041	12	CNS02BOY	AL190123 Tetradon
c 30	36	10.0	802	10	BG284658	BG284658 602408837
c 31	36	10.0	959	12	CNS06T7U	AL414208 T3 end of
c 32	35.4	9.9	599	9	AW966116	AW966116 EST378189
c 33	35.4	9.9	719	12	AQ969736	AQ969736 LERUP63TF
c 34	35.2	9.8	612	12	BH186623	BH186623 031_E-08-
c 35	35.2	9.8	612	12	CNS07R27	AL623569 T3 end of
c 36	35.2	9.8	658	10	BE823320	BE823320 GM700020B
c 37	35.2	9.8	1101	12	CNS0141H	AL103583 Drosophila
c 38	35	9.7	385	9	AA358198	AA358198 EST67073
c 39	35	9.7	706	12	AQ855359	AQ855359 CpG1892B
c 40	34.8	9.7	402	9	AI381291	AI381291 tc49f03.x
c 41	34.8	9.7	477	10	BI495304	BI495304 df116g07.
c 42	34.8	9.7	657	10	BE597274	BE597274 EST495952
c 43	34.8	9.7	703	10	BI495303	BI495303 df116g07.
c 44	34.8	9.7	783	10	BG934273	BG934273 SK1-0569
c 45	34.8	9.7	783	10	BG934273	BG934273 SK1-0569

ALIGNMENTS

RESULT 1
LOCUS AA056905 512 bp mRNA linear EST 18-SEP-1996
DEFINITION EST224F Pig Spleen lambda gt 11 library (Clontech Cat # PL1006b)
Sus scrofa cDNA clone SPL224 forward similar to L25259 C11A4
counter-receptor , human, mRNA sequence.

ACCESSION AA056905 GI:1549545
VERSION AA056905.1
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 512)
AUTHORS Tuglie,C.K., Wahls,S. and Schmitz,C.
TITLE Expressed Sequence Tags from Pig Spleen
JOURNAL Unpublished (1996)
COMMENT Contact: Tuglie CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ktuglie@iastate.edu

PCR Primers
FORWARD: TGCGCAGACTCTG
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location/Qualifiers
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BASE COUNT 125 a 106 c 114 g 163 t 4 others

AX002781	LOCUS	AX002781	738 bp	DNA	linear	PAT 21-AUG-2000
DEFINITION	Sequence 4 from Patent W09855607.					
ACCESSION	AX002781					
VERSION	AX002781.1	GI:9885109				
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct. synthetic construct. artificial sequence.					
REFERENCE	1 (bases 1 to 738)					
AUTHORS	Bebbington,C.R. and Carroll,M.W.					
TITLE	Vector					
JOURNAL	Patent: WO 9855607-A 4 10-DEC-1998; BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB)					
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BASE COUNT	215 a 168 c 148 g 207 t					
ORIGIN						
Query Match	30.6%; Score 110; DB 6; Length 738;					
Best Local Similarity	73.5%; Pred. No. 3.7e-19;					
Matches 169; Conservative	0; Mismatches 55; Indels 6; Gaps 2;					
OY 1	ATACAGGTTACCCAGAACCTTAAGACATGTAATTTTCAGCTTAACACTGAGACATTCAACT 60					
Db 460	ATACACGGTTACCCAGAACCTTAAGAGATGAGTGTGTTTGCCTAAGAACCAAGATTCAACT 519					
OY 61	ACTAAGTGTGATACGTCTATGACAGAAATCTGCAAAATATATATGACAGACTGTACACGTT 120					
Db 520	ATACAGTATGATGTGATTAATGACAGAAATCTCAGATTAATGTCACAGAACTGTACGACGTT 579					
OY 121	TCTATCAGCTTGCCCTTTTTCAGTCCCTGAG--CACACAAATGTGAGGCGCTTTTGTGCC 177					
Db 580	TTCATCAGCTTGCTGTGTTTCAATCCCTGATGTTCAGACAAATATGACCATCTTCTGTAAT 639					
OY 178	CTGAACACTGAGACACTGGAGATGTGCTGCCCTACCTTCAATATAGA 227					
Db 640	CTGGAACCTGACA---AGACGCGGCTTTTATCTTCACTTCTCTATAGA 686					
RESULT 13						
LOCUS	AX149548	738 bp	DNA	linear	PAT 08-JUN-2001	
DEFINITION	Sequence 9 from Patent W00136486.					
ACCESSION	AX149548					
VERSION	AX149548.1	GI:14347987				
KEYWORDS						
SOURCE						
ORGANISM	synthetic construct. synthetic construct. artificial sequence.					
REFERENCE	1 (bases 1 to 738)					
AUTHORS	Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W., Ellaid,F.M. and Myers,K.A.					
TITLE	Antibodies					
JOURNAL	Patent: WO 0136486-A 9 25-MAY-2001; Oxford Biomedica (UK) Limited (GB)					
FEATURES						
source	location/Qualifiers					
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	/db_xref="taxon:32630"					

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Best Local Similarity	73.5%; Pred. No. 3,7e-19;							
Matches 169; Conservative	0; Mismatches 55; Indels 6; Gaps 2;							
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Db	460	ATACAGCGTTACCCAGAACCTTAAGAGATGTGATTTTACGTAAAGAACCAAGAAATTCACCT	519					
QY	61	ACTAAGATGATTAAGTCATGATGAAGAAATCTCAAAATATATGACAGACAGATGTCAACGTT	120					
Db	520	ATGAGATATGATGATGATTTATGCAAGAAATCTCAAGATATATGTCACAGAACTGTACGACGTT	579					
QY	121	TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAG--CACACAATGTAGCGCTTTTGTGCC	177					
Db	580	TTCATCAGCTTGCTGTTCATTTCCCTGATGTACAGACATATAGACATTCATCTCTATT	639					
QY	178	CTGAACCTGGAGACACTGGAGATGTGTCTCCCTACCTTCAATATAGA	227					
Db	640	CTGGAACCTGACA--AGACGCGCTTTTATCTTCACCTTCTCTATAGA	686					
RESULT 14								
LOCUS	AR147737	751	bp	DNA	linear	PAT	08-AUG-2001	
DEFINITION	Sequence 34 from patent US 6225042.							
ACCESSION	AR147737							
VERSION	AR147737.1	GI:15111827						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 751)							
AUTHORS	Cal, Z., Sprent, J., Brunmark, A., Jackson, M., and Peterson, P. A.							
TITLE	Antigen presenting system and methods for activation of T-cells							
JOURNAL	Patent: US 6225042-A 34 01-May-2001;							
FEATURES	Location/Qualifiers							
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BASE COUNT	218	a	174	c	149	g	210	t
ORIGIN								
Query Match	30.6%; Score 110; DB 6; Length 751;							
Best Local Similarity	73.5%; Pred. No. 3,7e-19;							
Matches 169; Conservative	0; Mismatches 55; Indels 6; Gaps 2;							
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Db	484	ATACAGCGTTACCCAGAACCTTAAGAGATGTGATTTTCTTAAGAACCAAGAAATTCACCT	543					
QY	61	ACTAAGTATGATACTGTCAATGAGAAGAAATCTCAAAATATATGACAGACAGATGTCAACGTT	120					
Db	544	ATGAGATATGATGATGATTTATGCAAGAAATCTCAAGATATATGTCACAGAACTGTACGACGTT	603					
QY	121	TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAG--CACACAATGTAGCGCTTTTGTGCC	177					
Db	604	TTCATCAGCTTGCTGTTCATTTCCCTGATGTACAGACAAATATGACCAATCTCTCTATT	663					
QY	178	CTGAACCTGGAGACACTGGAGATGTGTCTCCCTACCTTCAATATAGA	227					
Db	664	CTGGAACCTGACA--AGACGCGCTTTTATCTTCACCTTCTCTATAGA	710					
RESULT 15								
LOCUS	AR159759	751	bp	DNA	linear	PAT	17-OCT-2001	
DEFINITION	Sequence 34 from patent US 6251627.							
ACCESSION	AR159759							
VERSION	AR159759.1	GI:16222532						
KEYWORDS								

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QY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 120
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Db 99603 ATCAGATATGATGTTATGACAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 99544

QY 121 TCTATCAGCTTGCTTTTTCAGTCCCGAAG---CACAAATGAGCGCTTTTGCC 177
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Db 99543 TCTATCAGCTTGCTTTTTCAGTCCCGAAG---CACAAATGAGCGCTTTTGCC 99484

QY 178 CTGAAGCTGAGA 190
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RESULT 11
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LOCUS AR112784
DEFINITION Sequence 46 from patent US 6130316.
ACCESSION AR112784
VERSION AR112784.1 GI:14092684
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Freeman,G.J., Nadler,L.M., Gray,G.S. and Greenfield,E.
TITLE Fusion proteins of novel CTLA4/CD28 ligands and uses therefore
JOURNAL Patent: US 6130316-A 46 10-OCT-2000;
FEATURES
source 1..306
location/Qualifiers
BASE COUNT 97 a 64 c 51 g 94 t
ORIGIN

Query Match 30.6%; Score 110; DB 6; Length 306;
Best Local Similarity 73.5%; Pred. No. 3.9e-19;
Matches 169; Conservative 0; Mismatches 55; Indels 6; Gaps 2;

QY 1 ATACAGGTTATCCAGACCTAAGAGATGATTTTACGCTAAACACTGAAATTAAC 60
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Db 79 ATACAGGTTATCCAGACCTAAGAGATGATTTTACGCTAAACACTGAAATTAAC 138

QY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 120
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Db 139 ATCAGATATGATGTTATGACAGAAATCTCAAAATATGTGACAGAACTGTACAACTT 198

QY 121 TCTATCAGCTTGCTTTTTCAGTCCCGAAG---CACAAATGAGCGCTTTTGCC 177
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Db 199 TCTATCAGCTTGCTTTTTCAGTCCCGAAG---CACAAATGAGCGCTTTTGCC 258

QY 178 CTGAAGCTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 227
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Db 259 CTGAAGCTGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGA 305

RESULT 12

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/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT      302 a      241 c      202 g      249 t
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Best Local Similarity 73.6%   Pred. No. 4,4e-23;
Matches 173; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

OY      1 ATACAGGTATCCCAAGCTAGAGATGATTTTCAGTCAACACTGAACTTAACCT 60
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      460 ACACAGAGCTACCCAGAACCCAGAGATGATATGTGTGTAATACAGAGATTCAC 519
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY      61 ACTAAGTGTGACTGATGATGAAGAAATCTCAAAATATGTGACAGACTGTCAACGTT 120
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      520 ACTGAGCATGATGCTGACATGAAATCTCAAAATCAATCAACGAGAACTCTCAATGTA 579
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY      121 TCTATCAGCTTGCTTTTTCAGTCCCTGAGACACACAAATGAGCGCTTTTGCCCTG 180
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      580 TCAATCAGAGGTGTCTCTTCCCATCCCTCCGAGACAAATGTGAGCAATCGTCTGTCTG 639
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
OY      181 AACTGAGAGACACTGAGAGA---TCCTGCTCTCCCTACCTTCAATATAGAAACCA 232
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB      640 CAACTTGAGCCAGACAGACACTCTTTTCTCTCCCTACCTTCAATATAGATGCAA 694
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RESULT 10
AC068630/164161 bp DNA linear PRI 01-NOV-2001
LOCUS      Homo sapiens 3 BAC RP11-289N10 (Roswell Park Cancer Institute Human
ACCESSION  AC068630
VERSION     AC068630
KEYWORDS    complete sequence.
SOURCE      human.
ORGANISM    human.
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
            1 (bases 1 to 164161)
            Muzny D.M., Adams C., Adio-Oduola B., Ali-osman F.R., Allen C.,
            Albrooks S.L., Amaratunga H.C., Are J.R., Banks R., Barberia J.,
            Benton J., Bivage K., Brown E., Brown M., Bryant N.P., Buhay C.,
            Butch P., Burkett C., Burrell K.L., Byrd N.C., Carron T.F.,
            Carter M., Cavazos S.R., Chacko J., Chavez D., Chen G., Chen R.,
            Chan Z., Chowdhry I., Christopoulos C., Cleveland C.D., Cox C.,
            Coyle M.D., Dathorne S.R., David R., Davila M.L., Davis C.,
            Davy-Carroll L., Dederich D.A., Delaney K.R., Delgado O.,
            Duan A.L., Ding Y., Dinh H.H., Douthwaite K.J., Drepper H.,
            Dugan Rocha S., Durbin K.J., Earnhart C., Edgar D., Edwards C.C.,
            Elhaj C., Escotto M., Falls T., Ferraguto D., Flagg N., Ford J.,
            Foster P., Frantz P., Gabisi A., Gao J., Garcia A., Garner T.,
            Garza N., Gill R., Gorrell J.H., Guevara M., Gunaratne P., Hale S.,
            Hamilton K., Harris C., Harris K., Hart M., Havlak P., Hawes A.,
            He X., Hernandez J., Hernandez O., Hodgson A., Hogues M.,
            Holloway C., Hollins B., Homai F., Howard S., Huber J., Jolly S.,
            Hume J., Jackson L.E., Jacobson B., Jia Y., Johnson R., Jolivet S.,
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            Lewis L., Li J., Li Z., Licharge O., Lieu C., Liu J., Liu W.,
            Louissege H., Lozado R.J., Lu X., Lucier A., Lucier R., Luna R.,
            Ma J., Maheshwari M., Mapa P., Martin R., Martindale A.,
            Martinez E., Massey E., Mawhney E., McLeod M.P., Meador M.,
            Mel G., Metzger M., Miner G., Miner Z., Mitchell T., Mohabhat K.,
            Moore S., Morgan M., Morris T., Morris S., Moser M., Neal D.,
            Nelson D., Newton J., Newton N., Nguyen A., Nguyen N., Nguyen N.,
            Nickerson E., Nwokenwo S., Ogih M., Okunou G., Oragunye N.,
            Oviedo R., Pace A., Payton B., Peery J., Perez L., Peters L.,
            Pickens R., Primus E., Pu L.L., Quiles M., Ran Y., Rivers M.,
            Rojas A., Rojubokan I., Rolfe M., Ruiz S., Severy G., Scherer S.,
            Scott G., Shen H., Shooshari N., Sisson I., Sodergren E.,
            Sonaike T., Sparks A., Stanley H., Stone H., Sutton A., Satek A.,
            Taber P., Tamerisa A., Tamerisa K., Tang H., Tansey J., Taylor C.,

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TITLE      Taylor T., Telirod B., Thomas N., Thomas S., Usmani K., Vasquez L.,
            Vera Y., Villalon D., Vinson R., Wall R., Wang S., Ward-Moore S.,
            Warren R., Washington C., Watlington S., Williams G.,
            Williamson A., Wlecczyk R., Wooden S., Worley K., Wu C., Wu Y.,
            Wu Y.F., Zhou J., Zorrilla S., Naylor S.L., Weinstein G. and
            Gibbs R.
REFERENCE   Direct Submission
AUTHORS     Unpublished
            2 (bases 1 to 164161)
TITLE      Worley K.C.
REFERENCE   Direct Submission
AUTHORS     Submitted (06-MAY-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 164161)
            Worley K.C.
            Direct Submission
            Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Nov 1, 2001 this sequence version replaced gi:16152225.
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STRs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT REPORT:

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FEATURES
source      location/qualifiers
            1. 164161
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="3"
            /clone="RP11-289N10"
            1. 1980
            /rpl_family="L1MA4"
            repeat_region
            2077. .2651
            /rpl_family="MER7C"
            repeat_region
            2661. .3430
            /rpl_family="L1ME3A"
            repeat_region
            3433. .3457
            /rpl_family="(TCTCCC)n"

```

TITLE Cloning and distribution of cattle CD86
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 924)
AUTHORS Brooke/G.P.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-2000) Brooke G.P., Cellular Immunology, Institute
For Animal Health, Compton, Berks, RG20 7NN, UNITED KINGDOM

FEATURES
Source
1..924
/organism="Bos taurus"
/db_xref="taxon:9913"
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/dev_stage="adult"
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72..924
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72..>924
/function="Immune response"
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/product="CD86 antigen"
/protein_id="CAC13140.1"
/db_xref="GI:10803380"
/translation="MRPKCTMDLRNIMGALRLSYKVFEGSASLKSHPENETGE
LPCRPMTOMLSDELVIETWQDNKLVIELFKGOKPNVNPVKYIGRTSPDQSWTL
RLHVOIKDGTSGYQCFTHRRSGLYSIHOMSDLIYANFOSPEIRLIANOTKESNI
INLTCSSIDGYPEPQRYVSLNNTNSSTIDAVKKSQSIITELVNVISVSRPIPE
TNVIFCALQLEPLKILISQPINIDKSPVSPVDPDHLIMIALLVVVSQWVLT
LKKKKKRL"

BASE COUNT 295 a 226 c 175 g 228 t
ORIGIN

Query Match 40.6%; Score 145.6; DB 4; Length 924;
Best Local Similarity 76.7%; Pred. No. 1e-28;
Matches 178; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 ATACAAGTTACCCAGACCTAAGAGATGATTTTTCAGCTAAGACCTGAGATTCACCT 60
DB 573 ATACAAGTTACCCAGACCTAAGAGATGATTTTTCAGCTAAGACCTGAGATTCACCT 632
QY 61 ACTAAGTATGATCTGTCATGAGAATCTCAAAATTAATGTCAGACAGCTACACGTT 120
DB 633 AGCACCATTGATGCTGTCATGAGAATCTCAAAATTAATGTCAGACAGCTACACGTT 692
QY 121 TCTATCAGCTGCTTTCAGTCCCTGAGACACAGATGAGCGCTTTTGCCCTG 180
DB 693 TCTATCAGCTGCTTTCAGTCCCTGAGACACAGATGAGCGCTTTTGCCCTG 752
QY 181 AAATCGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGAACCA 232
DB 753 CAACCTGAGCCAGACAGATATTTATCCCACTTCAATATAGATGACAA 804

RESULT 8
LOCUS PICCD86G 994 bp mRNA linear MAM 17-JUN-1997
DEFINITION Sus scrofa CD86 mRNA, complete cds.
ACCESSION L76099
VERSION L76099.1 GI:2198558
KEYWORDS T cell costimulation.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS Maher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and
Bothwell,A.L.
TITLE Porcine endothelial CD86 is a major costimulator of xenogeneic
human T cells: cloning, sequencing, and functional expression in
human endothelial cells
JOURNAL J. Immunol. 157 (9), 3838-3844 (1996)
MEDLINE 97047772

COMMENT GSDB:S:74002
FEATURES
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1..994
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/cell_type="endothelial"
/clone_lib="3"
/dev_stage="adult"
1..994
/gene="CD86"
1..978
/gene="CD86"
/standard_name="B7-2"
/note="putative"
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ORMVHLNNTKNTSTEDHADMKSQNNITELVNVISVSLPIPETNVSIVCLQEPS
KTLFSLPCNIDAKPPQPPVDPDHTIMIALLVVYVCGSVTLTKRKKKQGPS
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979..994
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/note="putative"
994
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/evidence="experimental"
evidence=experimental 249 t

BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN

Query Match 34.7%; Score 124.6; DB 4; Length 994;
Best Local Similarity 73.6%; Pred. No. 4.4e-23;
Matches 173; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATACAAGTTACCCAGACCTAAGAGATGATTTTTCAGCTAAGACCTGAGATTCACCT 60
DB 460 ACACAAGGCTACCCAGACCTAAGAGATGATTTTTCAGCTAAGACCTGAGATTCACCT 519
QY 61 ACTAAGTATGATCTGTCATGAGAATCTCAAAATTAATGTCAGACAGCTACACGTT 120
DB 520 ACTGAGCATATGCTGTCATGAGAATCTCAAAATTAATGTCAGACAGCTACACGTTA 579
QY 121 TCTATCAGCTGCTTTCAGTCCCTGAGACACAGATGAGCGCTTTTGCCCTG 180
DB 580 TCAATCAGGGGTCTCTTCCATCCCTCCGAGACAAATGTGACATGTGTGCTG 639
QY 181 AAATCGAGACACTGAG 232
DB 640 CAACCTGAGCCAGACAGACAGCTGCTTTCCTCCCTACCTGTAATATAGATGACAA 694

RESULT 9
LOCUS AX027016 994 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 13 from Patent WO00377102.
ACCESSION AX027016
VERSION AX027016.1 GI:10188045
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS Rogers,N.J., Dorling,A. and Lechler,R.I.
TITLE Immunosuppression
JOURNAL Patent: WO 0037102-A 13 29-JUN-2000;
ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;
LECHLER ROBERT IAN (GB)
FEATURES
Source
1..994
Location/Qualifiers

PUBMED 11491535
 REFERENCE 2 (bases 1 to 901)
 AUTHORS Villinger,F.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory University School of Medicine, Winship Cancer Institute, 1365B Clifton Rd, Atlanta, GA 30322, USA
 FEATURES
 source 1..901
 /organism="Papio cynocephalus anubis"
 /sub-species="anubis"
 /db_xref="taxon:9555"
 7..57
 7..834
 /note="B7.2"
 /product="CD86 protein precursor"
 /protein_id="AAK37532.1"
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 /translation="MGLSNILFVNAFLLSGAAPLIQAVENETADLPQFANSQNSRLSELVVFQNONENLVINEVYLGREKEDSVHSKMGRTSDPESWLRNLNQLKDKGLYOCIIHKRPQEMIRIHOVNSLSVLAISOPEIYISNITENMYINLGSIHGYPPEKMSVYLRTKSTTEIYDGVMSKODNTETLDVSLISVSPDYTSNMWTLPCVLETKTOLLSPESTINMERESQTKRKREKINPERSDEAQCVCFLKTPSCDKSDTHF"
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 BASE COUNT 281 a 193 c 178 g 249 t
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 Best Local Similarity 74.5%; Pred. No. 1.2e-38;
 Matches 272; Conservative 0; Mismatches 84; Indels 9; Gaps 3;
 QY 1 ATCAAGTTTACCAGAACTTAAGAGATGATTTTTCAGCTTAACCTGAGATTCAACT 60
 Db 466 ATACAGGTATTACCAAGAACTGAGAGATGATTTTCTTAAGAACCAAGATTCAACT 525
 QY 61 ACTAAGTATGATCTGTCTATGAAAGAAATCTCAAAATATGTGACAGAACTGACAACT 120
 Db 526 ATCGATATGATGATGTGTATGCAAAATCTCAAGATTAATGTACAGAACTGACAGCT 585
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 Db 586 TCCATAGCTTGCTTTTTCAGTCCCTGAAG---CACNCAATGTGAGCTCTTTTGTGCG 177
 QY 178 CTGAAGCTGGAGACACTGAGATGCTGCTCCCTCACTTCAATATAGAAACATCAAA 237
 Db 646 CTGGAAGCTGACA---AGACAGAGCTTTTATCTCTACCTTTCTTATAGAACCAACACA 702
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 QY 298 TCTGATGAGAGCCAGTG---TATTAACTTTTGAAGACAGCCTCAGGCGACAAAAGTACT 354
 Db 763 TCTGATGAGAGCCCAATGTGTTTAAAGTTGAAGACACCTTCATGCGACAAAAGTGAT 822
 QY 355 ACACA 359
 Db 823 ACACA 827
 RESULT 6
 LOCUS AF106826 1897 bp mRNA linear MAM 14-DEC-1999
 DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
 ACCESSION AF106826
 VERSION AF106826.1 GI:6572516
 KEYWORDS
 SOURCE dog.
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 1897)
 AUTHORS Yang,S. and Sim,G.K.
 TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules
 JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
 MEDLINE 2003996
 REFERENCE 2 (bases 1 to 1897)
 AUTHORS Yang,S. and Sim,G.-K.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA
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 /product="B7-2 protein"
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 QY 1 ATCAAGTTTACCAGAACTTAAGAGATGATTTTTCAGCTTAACCTGAGATTCAACT 60
 Db 486 ATACAGGTATTACCAAGAACTGAGAGATGATTTTGTGTAAGAACCGAGATTCAAGT 545
 QY 61 ACTAAGTATGATCTGTCTATGAAAGAAATCTCAAAATATGTGACAGAACTGACAACT 120
 Db 546 ACTAAGTATGATCTGTCTATGAAAGAAATCTCAAAATATGTGACAGAACTGACAACT 605
 QY 121 TCTATAGCTTGCTTTTTCAGTCCCTGAAGACACCAATGTGAGCGCTTTTGTGCGCTG 180
 Db 606 TCTATAGCTTGCTTTTTCAGTCCCTGAAGACACCAATGTGAGCGCTTTTGTGCGCTG 180
 QY 181 AAAGTGAAGACACTGAGATGCTGCTCTCCCTACCTTTCATATAGA 227
 Db 666 CAAGTGAAGACACTGAGATGCTGCTCTCCCTACCTTTCATATAGA 227
 RESULT 7
 LOCUS BTA291475 924 bp mRNA linear MAM 14-OCT-2000
 DEFINITION Bos taurus partial mRNA for CD86 antigen (CD86 gene).
 ACCESSION AJ291475
 VERSION AJ291475.1 GI:1080379
 KEYWORDS B7-2; CD86 antigen; CD86 gene.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 924)
 AUTHORS Brooke,G.P., Howard,C.J. and Parsons,K.R.

AUTHORS Nishimura, Y.
TITLE Direct Submission
JOURNAL Submitted (31-Jul-1999) Yorihiro Nishimura, Faculty of Agriculture,
The University of Tokyo, Department of Veterinary Microbiology;
1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan
(E-mail: yorihiro@vetero.ocn.ne.jp, Tel: +81-3-5841-5396,
Fax: +81-3-5841-8184)

COMMENT Sequence updated (08-Jun-2000).

FEATURES Location/Qualifiers

source

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/organism="Felis catus"

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/cell_type="peripheral blood mononuclear cell"

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240..1238

/gene="CD86"

CDS

240..1238

/gene="CD86"

/codon_start=1

/product="B-lymphocyte activation antigen B7-2 (CD86)"

/protein_id="BAB11688.1"

/db_xref="GI:9796388"

/translation="MGICDSTMGSLHTLLVAMALLSGVSSMKSOAYFNKTELPCHFT
NSONISLDELIVFMODDKLYLVEIFRKGKPNQVHLKYKGRSPDKDMNTRLRHVVO
IKDKGYHCFTIHYKPKGLVPMHOMSDSLVLANFSQPELTVTSNRTEMSGIINLCS
SIOGYPEPKEMFQDLNENSTTKYDVTVMKKSQNNVTELYNSISLPSVPEAHNVSVF
CALKLELLEMLSLPFINDAQPKDKDEQGHFLVIAVLVMEVFVFCGWSFKTLRKRK
KKQPSHECETIKRERESKQNERVPHYHVERSDAOCINILKTAAGDKSTTHF"

polya_signal

1245..1250

BASE COUNT

378 a 281 c 260 g 351 t

ORIGIN

Query Match

Best Local Similarity 63.3%; Score 227.2; DB 4; Length 1270;

Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 60

DB 723 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGAGATTCAACT 782

QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTGTT 120

DB 783 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTGTT 842

QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGAGCGCTTTTGTGCCCTG 180

DB 843 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGAGCGCTTTTGTGCCCTG 902

QY 181 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCATCAAAAG 240

DB 903 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGATGACACAACTAAG 962

QY 241 GAGAGAAA 248

DB 963 GATTAAGA 970

RESULT 4

LOCUS AY007704

DEFINITION Felis catus CD86 (CD86) mRNA, complete cds.

ACCESSION AY007704

VERSION AY007704.1

KEYWORDS GI:15418725

SOURCE

cat.

ORGANISM

Felis catus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE

1 (bases 1 to 2830)

AUTHORS Yang, S., Sellins, K.S., Powell, T., Stoneman, E., and Sim, G.K.

TITLE Novel transcripts encoding secreted forms of feline CD80 and CD86

JOURNAL Vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)

MEDLINE 21390213

PUBMED 11498243

REFERENCE 2 (bases 1 to 2830)

AUTHORS Yang, S.

TITLE Direct Submission

JOURNAL Submitted (06-Sep-2000) Immunology, Heska Corporation, 1613

Prospect Parkway, Ft Collins, CO 80525, USA

FEATURES Location/Qualifiers

source

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/organism="Felis catus"

/db_xref="taxon:9685"

gene

1..2830

/gene="CD86"

CDS

179..1177

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BASE COUNT

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ORIGIN

Query Match

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Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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DB 662 ATACAGGTTACCCAGAACCTAAGAGATGTTTTCAGCTAAACACTGGAATTCAACT 721

QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTGTT 120

DB 722 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGTCAGACAGACTGACAACTGTT 781

QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGAGCGCTTTTGTGCCCTG 180

DB 782 TCTATCAGCTTGCCTTTTTCAGTCCCTGAGACACAAATGAGCGCTTTTGTGCCCTG 841

QY 181 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGAAACCATCAAAAG 240

DB 842 AAACGTGAGACACTGGAGATGCTGCTCCCTACCTTCAATATAGATGACACAACTAAG 901

QY 241 GAGAGAAA 248

DB 902 GATTAAGA 909

RESULT 5

LOCUS AF344836

DEFINITION Papio cynocephalus anubis CD86 protein precursor, mRNA, complete

cds.

ACCESSION AF344836

VERSION AF344836.1

KEYWORDS GI:13649983

SOURCE

olive baboon.

ORGANISM

Papio cynocephalus anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecinae; Papio.

REFERENCE

1 (bases 1 to 901)

AUTHORS Villinger, F., Bostlik, P., Mayne, A.E., King, C.L., Genain, C.P.,

Weiss, W.R., and Ansari, A.A.

TITLE Cloning, sequencing, and homology analysis of nonhuman primate

Fas/Fas-ligand and co-stimulatory molecules

JOURNAL Immunogenetics 53 (4), 315-328 (2001)

MEDLINE 21383618

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547 ACTAGTATGATCTGTCATGAGAAATCTCAAAATATATGACAGAACTGTACACGTT 606
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121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
|||||
607 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 666
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181 AAACGAGACACATGAGATGCTGCTCCCTACCTTTTCAATATAGAAACATCAAAAG 240
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667 CAACCTGAGTCAAT---GAGCTTCCTCCCTACCTTATATATAGAAACATCAAAAGTG 723
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241 GAGAGAAAAGAGACAAACAGACCAAGAGAGTACCATACAGTACCTGAGAGATCT 300
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724 GAGAGAAAAGAGACAAACAGACCAAGAGAGTACCATACAGTACCTGAGAGATCT 783
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301 GATGAAGCCCACTGATTAACATTTTGAAGACAGCTTCAGGCGACAAAGACTACAC 359
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LOCUS AF157827
DEFINITION Felis catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
ORGANISM
cat.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
AUTHORS
1 (bases 1 to 1138)
Choi, I.-S., Hash, S.M., Winslow, B.J. and Collis, E.M.
Sequence analyses of feline B7 costimulatory molecules
JOURNAL
20180222 Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE
PUBMED 10713336

REFERENCE 2 (bases 1 to 1138)
AUTHORS
Choi, I.-S., Hash, S.M., Winslow, B.J. and Collis, E.M.
TITLE
Direct Submission
JOURNAL
Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 km. 222, College Station, TX 77843, USA
FEATURES
Location/Qualifiers
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/organism="Felis catus"
/db_xref="taxon:9685"
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/gene="CD86"
63..1052
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/note="B7-2 antigen"
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Best Local Similarity 94.8% Pred. No. 1.3e-50;
Matches 235; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 180
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666 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACAAATGTGAGCGTCTTTTGCCCTG 725
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181 AAACGAGACACATGAGATGCTGCTCCCTACCTTTTCAATATAGAAACATCAAAAG 240
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241 GAGAGAAA 248
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786 GATGAAGA 793
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RESULT 3
AB030652 1270 bp mRNA linear MAM 01-MAR-2001
LOCUS AB030652
DEFINITION Felis catus mRNA for B-lymphocyte activation antigen B7-2 (CD86),
complete cds.
ACCESSION AB030652
VERSION AB030652.1 GI:9796387
KEYWORDS
SOURCE
ORGANISM
Felis catus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
AUTHORS
1 (sites)
Nishimura, Y., Shimomura, M., Miyazawa, T., Sato, E., Nakamura, K.,
Izumiya, Y., Ikeda, Y., Mikami, T. and Takahashi, E.
Molecular cloning of the cDNAs encoding the feline B-lymphocyte
activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
interact with human CTLA-19
JOURNAL
20485322 Eur. J. Immunogenet. 27 (5-6), 427-430 (2000)
MEDLINE
REFERENCE 2 (bases 1 to 1270)

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 491.57 Seconds
(without alignments) 15282.914 Million cell updates/sec

Title: US-09-646-561-33

Perfect score: 359
Sequence: 1 atacaaggtaccaccagaacc.....gagcagacaaagtactacaca 359

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
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- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
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- 14: gb_vl:*
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- 26: em_ro:*
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- 31: em_htg_hum:*
- 32: em_htg_inv:*
- 33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	271	75.5	1795	4	AF106827	AF106827 Canis fam
2	227.2	63.3	1138	4	AF157827	AF157827 Felis cat
3	227.2	63.3	1270	4	AB030652	AB030652 Felis cat
4	227.2	63.3	2830	4	AY007704	AY007704 Felis cat
5	182.6	50.9	901	4	AF344836	AF344836 Papio cyn
6	169.4	47.2	1897	4	AF106826	AF106826 Canis fam
7	145.6	40.6	924	4	BT291475	BT291475 Bos tauru
8	124.6	34.7	994	4	PIGCD866	PIGCD866 Sus scrofa
9	124.6	34.7	994	6	AX027016	AX027016 Sequence
10	111.4	31.0	164161	6	AC068630	AC068630 Homo sapi
11	110	30.6	306	6	AR112784	AR112784 Sequence
12	110	30.6	738	6	AX002781	AX002781 Sequence
13	110	30.6	738	6	AX149548	AX149548 Sequence
14	110	30.6	751	6	AR147737	AR147737 Sequence
15	110	30.6	751	6	AR159759	AR159759 Sequence
16	110	30.6	751	6	AR160451	AR160451 Sequence
17	110	30.6	972	6	AX027005	AX027005 Sequence
18	110	30.6	1002	6	AR147736	AR147736 Sequence
19	110	30.6	1002	6	AR159758	AR159758 Sequence
20	110	30.6	1002	6	AR160450	AR160450 Sequence
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22	110	30.6	1048	9	AF344857	AF344857 Macaca mu
23	110	30.6	1062	9	AF344861	AF344861 Cercopit
24	110	30.6	1112	9	HUMB72A	L25259 Human CTLA4
25	110	30.6	1120	6	AR030780	AR030780 Sequence
26	110	30.6	1120	6	AR112747	AR112747 Sequence
27	110	30.6	1120	6	AR146413	AR146413 Sequence
28	110	30.6	1120	6	AX047043	AX047043 Sequence
29	110	30.6	1161	6	AR146414	AR146414 Sequence
30	110	30.6	1424	6	AX330924	AX330924 Sequence
31	110	30.6	1424	6	AX332506	AX332506 Sequence
32	110	30.6	1424	6	HSU04343	U04343 Human CD86
33	110	30.6	2205	6	AX188198	AX188198 Sequence
34	109.8	30.6	737	9	HSB725	U17719 Human CTLA-
35	106.8	29.7	1062	9	AF344840	AF344840 Cercopitu
36	102	28.4	1156	4	RABCD86B	D49842 Rabbit mRNA
37	85	23.7	133	4	AF222915	AF222915 Sus scrofa
38	78	21.7	210	6	AR146418	AR146418 Sequence
39	77.2	21.5	418	10	MMB72608	U39463 Mus muscu
40	77.2	21.5	930	6	AX027012	AX027012 Sequence
41	77.2	21.5	984	10	AF065897	AF065897 Mus muscu
42	77.2	21.5	984	10	AF065898	AF065898 Mus muscu
43	77.2	21.5	984	10	AF065900	AF065900 Mus muscu
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ALIGNMENTS

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1795)
AUTHORS
TITLE
New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
JOURNAL
Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE
20093996
REFERENCE
2 (bases 1 to 1795)
AUTHORS
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
FEATURES
Location/Qualifiers

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1134
US-08-702-525-24

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Best Local Similarity 69.0%; Pred. No. 9e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

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QY 61 ACTAAGTATGATCTGATGAGAAATCTCAAAATATGTGACAGACTGTACACGTT 120
DB 685 ATGAGTATGATGATTTATGACAGAAATCTCAAGATATGTCACAGAACTGTACGAGTT 744
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DB 745 TCCATCAGCTTGTCTGTTTATTCCTGATGTTACGACAAATATGCAATCTTGTATTT 804
QY 178 CTGAAGCTGAGACACTGAGATGCTCTCCCTACCTTTCATATATGATGCACAACT 237
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QY 238 AAGATTAAGACCTTGACAGAGCCACTTCTGATGATTCGGCTGTACTTGTATGTTT 297
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QY 358 GGGCCCTCTCATGATGTGAACATCAAAAGGAGAGAAAGAGAGAGAGAGAGCC 417
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QY 475 TTGAAGACAGCTGAGCGGACAAAAGTACTACA 507
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RESULT 15

PCT-US95-02576-24
Sequence 24, Application PC/TUS9502576

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules

TITLE OF INVENTION: and Uses Therefor

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02576

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1134
PCT-US95-02576-24

Query Match 41.8%; Score 212.6; DB 5; Length 1161;
Best Local Similarity 69.0%; Pred. No. 9e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

QY 1 ATACAGGTTACCCAGACCTTAAGAGATGATTTTACCTTAACCTGAGAATTCACCT 60
DB 625 ATACAGGTTACCCAGACCTTAAGAGATGATTTTACCTTAACCTGAGAATTCACCT 684
QY 61 ACTAAGTATGATCTGATGAGAAATCTCAAAATATGTGACAGACTGTACACGTT 120
DB 685 ATGAGTATGATGATTTATGACAGAAATCTCAAGATATGTCACAGAACTGTACGAGTT 744
QY 121 TCTATCAGCTTGGCTTTTTCAGTCCCTGAAG--CACACAATGTAGCGCTTTTGTGCC 177
DB 745 TCCATCAGCTTGTCTGTTTATTCCTGATGTTACGACAAATATGCAATCTTGTATTT 804
QY 178 CTGAAGCTGAGACACTGAGATGCTCTCCCTACCTTTCATATATGATGCACAACT 237
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DB 1036 AAAAGAGAAAAATCCATATACCTGAAAGATCTGATGAGAGAGAGAGAGAGAG 1095
QY 475 TTGAAGACAGCTGAGCGGACAAAAGTACTACA 507
DB 1096 TCGAAGACATCTTCATGCGACAAAAGTACTACA 1128

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Job time : 30.6516 secs

APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-403-253A-3

Query Match 41.8%; Score 212.6; DB 4; Length 1120;
Best Local Similarity 69.0%; Pred. No. 8.8e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

OY 1 ATACAGGTATCCAGAACCTAAGAGATGATATTTTCAGCTAAACATGATTCACCT 60
DB 584 ATACAGGTATCCAGAACCTAAGAGATGATATTTTCAGCTAAACATGATTCACCT 643
OY 61 ACTAAGTATGATGTCATGATGAGAAATCTCAAAATATGATGACAGACTGTACAGCTT 120
DB 644 ATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAAG--CACACAATGAGGCGCTTTTGTGCC 177
DB 704 TCCATCAGCTTGTCTGTTTTCATTCCTGATGTTACGACATATGACCATCTTCTGAT 763
OY 178 CTGAAGCTGAGACATGAGAGATGCTCTCTCCCTACCTTTCAATATGATGACACCT 237
DB 764 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAG-----AGCTT 814
OY 238 AAGGATAAAGACCTGGAACAGGCACTTCCTGATGATGAGGCTGATGATGATGAT 297
DB 815 GAGGACCTGACGCTCCCGGACGACATTCCTTGATGATGATGATGATGATGATGATGAT 874
OY 298 GTTGTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 357
DB 875 ATTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 934
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DB 935 CGCAACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 994
OY 418 GAAGATACATACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
DB 945 AAAAGAGAAAAATCCATATACCTGGAAGATGATGATGATGATGATGATGATGATGATGAT 1054

OY 475 TTGAAGACAGCTTCAGGCGACAAAGTACTACA 507
DB 1055 TCGAAGACATCTTCATGCGACAAAGTACTACA 1087

RESULT 12
PCT-US95-02576-22
Sequence 22, Application PC/TUS9502576
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
PCT-US95-02576-22

Query Match 41.8%; Score 212.6; DB 5; Length 1120;
Best Local Similarity 69.0%; Pred. No. 8.8e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

OY 1 ATACAGGTATCCAGAACCTAAGAGATGATATTTTCAGCTAAACATGATTCACCT 60
DB 584 ATACAGGTATCCAGAACCTAAGAGATGATATTTTCAGCTAAACATGATTCACCT 643
OY 61 ACTAAGTATGATGTCATGATGAGAAATCTCAAAATATGATGACAGACTGTACAGCTT 120
DB 644 ATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703
OY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAAG--CACACAATGAGGCGCTTTTGTGCC 177
DB 704 TCCATCAGCTTGTCTGTTTTCATTCCTGATGTTACGACATATGACCATCTTCTGAT 763
OY 178 CTGAAGCTGAGACATGAGAGATGCTCTCTCCCTACCTTTCAATATGATGACACCT 237
DB 764 CTGGAACCTGACA--AGACGCGGCTTTTATCTTCACCTTCTCTATAG-----AGCTT 814
OY 238 AAGGATAAAGACCTGGAACAGGCACTTCCTGATGATGAGGCTGATGATGATGATGAT 297
DB 815 GAGGACCTGACGCTCCCGGACGACATTCCTTGATGATGATGATGATGATGATGATGATGAT 874


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1      FILING DATE: 28-AUG-1993
2      APPLICATION NUMBER: 08/101,624
3      FILING DATE: 26-JULY-1993
4      APPLICATION NUMBER: 08/147,773
5      FILING DATE: 3-NOV-1993
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Mandragouras, Amy E.
8      REGISTRATION NUMBER: 36,207
9      REFERENCE/DOCKET NUMBER: RPT-004CP3
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: (617) 227-7400
12     TELEFAX: (617) 227-5941
13     INFORMATION FOR SEQ ID NO: 1:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 1120 base pairs
16     TYPE: nucleic acid
17     STRANDEDNESS: single
18     TOPOLOGY: linear
19     FEATURE:
20     NAME/KEY: CDS
21     LOCATION: 107..1093
22     US-08-479-744A-1
23
24     Query Match 41.8%; Score 212.6; DB 3; Length 1120;
25     Best Local Similarity 69.0%; Pred. No. 8,86-57;
26     Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps
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28     QY 1 ATCAAGAGTTACCCCAACCTTAAGAGAGTATTTTCAGCTAAACACTGGAATTCACCT 60
29     DB 584 ATACACGGTATACCAACCTTAAGAGAGTATTTTCAGCTAAACACTGGAATTCACCT 643
30     QY 61 ACTAGTATGATACCTGTCATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAAGCTT 120
31     DB 644 ATGAGATGATGATGATGATATATGACAGAAATCTCAAAATAATGTGACAGAACTGTACAAGCTT 703
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33     DB 704 TCCATACGCTTGCCTTTTTCATTCCTGATGTTACGACCAATTAAGACATCTTCTGATAT 763
34     QY 178 CTGAACCTGAGACACATGAGAGATGCTGCTCTCCCTACCTTCATTAATAGATGACAACT 237
35     DB 764 CTGGAACAGTACAC---AGACGGGCTTTTATCTTCACCTTCTCTATAG-----AGCTT 814
36     QY 238 AAGGATTAAGAACCCCTGACACAGGCCACTTCCCTGEGATTGCGGCTGTACTTGAATGTTT 297
37     DB 815 GAGGAGCCCTGAGCTCTCCCGACAGCCACATCTCCTTGAGATTACAGCTGTACTTCCAAAGTT 874
38     QY 298 GTTGTTTTTGTGGATGGTGTGCTTTTAAACACATAAGGAAAGGAAGGAAGGACGCT 357
39     DB 875 ATTATATATGTGTATGTTTCTTCTTAATTTCTATGGAATGGAAGAAAGGACGCT 934
40     QY 358 GGCCCTCTCATGATGTAAGAACATCAAAAGGAGAGAGAAAAGAGACAAACAGACCAAC 417
41     DB 935 CGCAACTCTTATTAATAGTGAACCAACAAATGAGAGGAAGAGAGATGGAACAGACCAAG 994
42     QY 418 GAAGAGTACATACACAGTACTTCTAGAGATCTGATGAAGCCCACTG---TATTAACTTT 474
43     DB 995 AAAGAAGAAAAATCCATTAATACCTTAAGAAGATCTGATGAAGCCCACTGTTTAAAAAGT 1054
44     QY 475 TTGAAGACAGCCTCAGGCGACAAAGATCTACCA 507
45     DB 1055 TCGAAGACATCTTCATGCGACAAAGATATACA 1087
46
47     RESULT 8
48     US-08-280-757B-1
49     ; Sequence 1, Application US/08280757B
50     ; Patent No. 6130316
51     ; GENERAL INFORMATION:
52     ; APPLICANT: Freeman, Gordon J.
53     ; APPLICANT: Nadler, Lee M.
54     ; APPLICANT: Gray, Gary S.

```


OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,641
FILING DATE: 8-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-641-33

Query Match 41.8%; Score 212.6; DB 4; Length 1002;
Best Local Similarity 69.0%; Pred. No. 8.4e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

QY 1 ATACAAGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAAATTCACCT 60
DB 484 ATACACGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAAATTCACCT 543
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGATGACAGAACTGTACACGTT 120
DB 544 ATCAGATATGATGTTATATGACAAATCTCAAGATATGTCACAGAACTGTACAGGTT 603
QY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAAG---CACAAATGTGACGCTTTTGTGCC 177
DB 604 TCCATCAGCTGCTTTTTCAGTCCCTGAATGTTACGAAATGACCAATCTCTGTATT 663
QY 178 CTGAACCTGAGACATGAGATGCTGCTCCTTCCCTACCTTTCATATATGATGACACCT 237
DB 664 CTGAAACTGACA---AGACGGGCTTTTATCTTACCTTTCTCTATAG-----AGCTT 714
QY 238 AAGATAAAGACCTGGAACAAGGCCACTTCTGTGATTCGGCTGTACTTGTATGTTT 297
DB 715 GAGGACCTCAGCTCCCGACAGACACATTCCTGTGATTCAGCTGTACTTCCACAGTT 774
QY 298 GTTCTTTTGTGGATGCTGCTCTTAAACACTAAGGAAAGAAAGAAAGACGCT 357
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QY 358 GGCCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
DB 835 CGCACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 418 GAAAGATACCATACCAAGTACCTGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAG 474
DB 895 AAAAGAGAAAGAAATCATATACCTGGAAGATGATGATGATGATGATGATGATGATG 954
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DB 955 TCGAAGACATCTTCATGCGACAAAGATGATACA 987

RESULT 4
US-09-039-762A-33
Sequence 33, Application US/09039762A
Patent No. 6255073
GENERAL INFORMATION:
APPLICANT: Cal, Zelig
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders

APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6255073th Wacker Drive, 36th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-039-762A-33

Query Match 41.8%; Score 212.6; DB 4; Length 1002;
Best Local Similarity 69.0%; Pred. No. 8.4e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;

QY 1 ATACAAGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGATTCACCT 60
DB 484 ATACACGGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGATTCACCT 543
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGATGACAGAACTGTACACGTT 120
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QY 121 TCTATCAGCTGCTTTTTCAGTCCCTGAAG---CACAAATGTGACGCTTTTGTGCC 177
DB 604 TCCATCAGCTGCTTTTTCAGTCCCTGAATGTTACGAAATGACCAATCTCTGTATT 663
QY 178 CTGAACCTGAGACATGAGATGCTGCTCCTTCCCTACCTTTCATATATGATGACACCT 237
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QY 238 AAGATAAAGACCTGGAACAAGGCCACTTCTGTGATTCGGCTGTACTTGTATGTTT 297
DB 715 GAGGACCTCAGCTCCCGACAGACACATTCCTGTGATTCAGCTGTACTTCCACAGTT 774
QY 298 GTTCTTTTGTGGATGCTGCTCTTAAACACTAAGGAAAGAAAGAAAGACGCT 357
DB 775 ATTATATGATGATGTTTCTGTCTAATCTCTATGAAATGGAAGAAAGAAAGCGGCT 834
QY 358 GGCCCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
DB 835 CGCACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 418 GAAAGATACCATACCAAGTACCTGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAG 474

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 : Search time 17.6516 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-30

Perfect score: 509

Sequence: 1 atacaaggtaccagacc.....ggcgacaaagtactacaca 509

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	212.6	41.8	972	4	US-08-848-760B-11	Sequence 11, Appl
2	212.6	41.8	1002	4	US-09-039-882A-33	Sequence 33, Appl
3	212.6	41.8	1002	4	US-09-039-641-33	Sequence 33, Appl
4	212.6	41.8	1002	4	US-09-039-762A-33	Sequence 33, Appl
5	212.6	41.8	1120	2	US-08-456-104-1	Sequence 1, Appl
6	212.6	41.8	1120	2	US-08-101-624-1	Sequence 1, Appl
7	212.6	41.8	1120	3	US-08-479-744A-1	Sequence 1, Appl
8	212.6	41.8	1120	3	US-08-280-757B-1	Sequence 1, Appl
9	212.6	41.8	1120	4	US-08-205-697A-22	Sequence 22, Appl
10	212.6	41.8	1120	4	US-08-702-525-22	Sequence 22, Appl
11	212.6	41.8	1120	4	US-08-403-253A-3	Sequence 3, Appl
12	212.6	41.8	1120	5	PCT-US95-02576-22	Sequence 22, Appl
13	212.6	41.8	1161	4	US-08-205-697A-24	Sequence 24, Appl
14	212.6	41.8	1161	4	US-08-702-525-24	Sequence 24, Appl
15	212.6	41.8	1161	5	PCT-US95-02576-24	Sequence 24, Appl
16	212.6	41.8	1424	5	US-09-326-186B-226	Sequence 226, App
17	212.6	41.8	1424	5	PCT-US94-09642-1	Sequence 46, Appl
18	110	21.6	306	3	US-08-479-744A-46	Sequence 46, Appl
19	110	21.6	306	3	US-08-280-757B-46	Sequence 46, Appl
20	110	21.6	751	4	US-09-039-882A-34	Sequence 34, Appl
21	110	21.6	751	4	US-09-039-641-34	Sequence 34, Appl
22	110	21.6	751	4	US-09-039-762A-34	Sequence 34, Appl
23	99	19.4	210	4	US-08-205-697A-31	Sequence 31, Appl
24	99	19.4	210	4	US-08-702-525-31	Sequence 31, Appl
25	99	19.4	210	5	PCT-US95-02576-31	Sequence 31, Appl
26	77.2	15.2	1151	4	US-08-456-104-3	Sequence 3, Appl
27	77.2	15.2	1151	4	US-08-205-697A-20	Sequence 20, Appl

28	77.2	15.2	1151	4	US-08-702-525-20	Sequence 20, Appl
29	77.2	15.2	1151	5	PCT-US95-02576-20	Sequence 20, Appl
30	77.2	15.2	1163	3	US-08-479-744A-22	Sequence 22, Appl
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32	77.2	15.2	1261	4	US-08-205-697A-12	Sequence 12, Appl
33	77.2	15.2	1261	4	US-08-702-525-12	Sequence 12, Appl
34	77.2	15.2	1261	5	PCT-US95-02576-12	Sequence 12, Appl
35	37.2	7.3	7218	1	US-08-232-463-14	Sequence 14, Appl
36	32.6	6.4	9048	3	US-08-973-273-4	Sequence 4, Appl
37	31.4	6.2	2935	1	US-08-246-583-1	Sequence 1, Appl
38	31.2	6.1	740	4	US-09-342-681C-99	Sequence 99, Appl
39	31	6.1	12047	2	US-09-022-461-1	Sequence 1, Appl
40	30	5.9	2351	4	US-09-276-531-3	Sequence 3, Appl
41	30	5.9	4865	3	US-08-894-017-24	Sequence 24, Appl
42	29.6	5.8	685	4	US-09-227-357-100	Sequence 100, App
43	29.6	5.8	1813	5	PCT-US94-12883-3	Sequence 3, Appl
44	29.6	5.8	3138	1	US-07-867-106-4	Sequence 4, Appl
45	29.6	5.8	14753	4	US-09-821-726-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-848-760B-11
Sequence 11, Application US/08848760B
Patent No. 6248721
GENERAL INFORMATION:
APPLICANT: Chang, Lung-Ji
TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Saliwanhik, Lloyd & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: United States of America
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,760B
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,702
FILING DATE: 09-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: PACE, DORAN R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CNG-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-5800
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-848-760B-11
Query Match 41.8%; Score 212.6; DB 4; Length 972;
Best Local Similarity 69.0%; Pred. No. 8.3e-57;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;
QY 1 ATCAAGGTTACCAACCTAAGGAGATGTATTTCAGCTAAACACTGAGATTCACT 60

DR WPI: 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1, Page 101-102; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1897 BP; 529 A; 383 C; 400 G; 585 T; 0 other;
Query Match 72.7%; Score 369.8; DB 20; Length 1897;
Best Local Similarity 85.7%; Pred. No. 8.1e-102;
Matches 436; Conservative 0; Mismatches 67; Indels 6; Gaps 2;
OY 1 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTAACTGAAATTCACACT 60
DB 1412 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTAACTGAAATTCACAGT 1353
OY 61 ACTAGTATGATCTGCTCATGAGAAATCTCAAAATATGTCAGACAACTGTACACGTT 120
DB 1352 ACTAGTATGATCTGCTCATGAGAAATCTCAAAATATGTCAGACAACTGTACACGTT 1293
OY 121 TCTATCAGCTGCTGCTTTTTCAGTCCCTGAGACACACATGTGAGCGCTTTTGTCCCTG 180
DB 1292 TCTATCAGCTGCTGCTTTTTCAGTCCCTGAGACACACATGTGAGCGCTTTTGTCCCTG 1233
OY 181 AAACGTGAGACATGAGATGCTGCTGCTTACCTTTCATATGATGACACATCTAG 240
DB 1232 CAACCTGAGTCAAT---GAAGCTTCCCTCCCTACCTTATATATAGATGACACA---TACG 1179
OY 241 GATAAAGACCTGAGAACAGGCACTTCTCTGATTCGCGCTGTACTGTAAATGTTTGT 300
DB 1178 AAACCCACCCCTGATGAGACACACATCTGATGTCGGCTGTGTAATGTGCTC 1119
OY 301 GTTTTGTGGAGTGTGCTCTTAAACACTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 1118 ATTTTGTGGAGTGTGCTCTTAAACACTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1059
OY 361 CCTCTCATGATGTGAACCATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 1058 CCTCTCATGATGTGAACCATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
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OY 481 ACAGCCTCAGGCGAG 509
DB 938 ACAGCCTCAGGCGAG 910
RESULT 13
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XX AAAA9661;
XX
XX 25-SEP-2000 (first entry)
XX
XX Pig costimulatory molecule CD86 (B7-2) cDNA.
XX
XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
KM xerotransplantation; organ transplant; vaccine; ss.
XX

OS Sus scrofa.
XX
XX Key Location/Qualifiers
XX CDS 36..1013
XX FT /*tag= a
XX
XX WO200037102-A2.
XX
XX 29-JUN-2000.
XX
XX 17-DEC-1999; 99WO-GB04200.
XX
XX 19-DEC-1998; 98GB-0027921.
XX
XX 23-OCT-1999; 99GB-0025015.
XX
XX (MLML-) ML LAB PLC.
XX
XX Lechler RI, Rogers NJ, Dorrling A.
XX
XX WPI: 2000-442537/38.
XX
XX P-PsDB; AAY95321.
XX
XX
XX Novel methods for improving tolerance to a xenograft comprising
PT immunizing a mammal with a T-cell epitope and a B-cell epitope -
PS disclosure; Fig 3; 81pp; English.
XX
XX The present sequence is that of cDNA clone CD86(1), which encodes
CC pig co-stimulatory molecule CD86 (B7-2) (see AAY95321). The clone
CC was obtained by PCR amplification of pig cDNA using primers (see
CC AAY9662-63) based on a published pig B7-2 sequence. The invention
CC relates to a novel strategy to inhibit costimulation by porcine
CC cells of human T cells, with particular importance in the context
CC of xerotransplantation of porcine organs. Recipients are immunised
CC with hybrid synthetic peptides comprising a T cell epitope
CC conjugated to sequences of the porcine costimulatory molecules
CC CD80, CD86 or CD40. Peptides that induce antibodies specific for
CC regions of costimulatory molecules involved in binding to their
CC counter-receptors on human cells (CD28 and CD14) are capable of
CC blocking the delivery of costimulation. Once the antibody response
CC has been induced, the transplanted organ will recall this response
CC due to the expression of the costimulatory molecules, thereby
CC sustaining the response, and providing an endogenous mechanism of
CC costimulatory blockade. The method is useful for improving the
CC tolerance of a host to xenografts, particularly porcine pancreatic
CC islet cells.
XX
SQ Sequence 1050 BP; 305 A; 260 C; 227 G; 258 T; 0 other;
Query Match 52.8%; Score 268.8; DB 21; Length 1050;
Best Local Similarity 75.5%; Pred. No. 2.6e-71;
Matches 391; Conservative 0; Mismatches 112; Indels 15; Gaps 4;
OY 1 ATACAGGTTACCCAGACCTAGAGATGATTTTCAGCTAACTGAAATTCACACT 60
DB 495 ACACAGGCTACCCAGACCTAGAGATGATTTTCAGCTAACTGAAATTCACACT 554
OY 61 ACTAGTATGATCTGCTCATGAGAAATCTCAAAATATGTCAGACAACTGTACACGTT 120
DB 555 ACTAGTATGATCTGCTCATGAGAAATCTCAAAATATGTCAGACAACTGTACACGTT 614
OY 121 TCTATCAGCTGCTGCTTTTTCAGTCCCTGAGACACACATGTGAGCGCTTTTGTCCCTG 180
DB 615 TCAATCAGGCTGCTGCTTCCATCCCTCCGAGACAAATGTGAGCATGCTGTGCTCG 674
OY 181 AAACGTGAGACATGAG 237
DB 675 CACTTGAAGCAAGACACTGCTTTTTCCTCCTGCTTGAATATGATGACAAAGCA 734
OY 238 AAGGATTAAGACCTGAGACAGGCACTTCTCTGATGAGCGCTGATGATGATGATGATG 297
DB 735 CCGTGCAACCCCGTGTCCAGACACACATCTGATGATGAGCTGATGATGATGATGATG 794

Db	387	TCATACACCTTGTCTCTTGTAGTCCCTGGAAAGCAAGCAATGTGAGCAATCTTCTGTGTCTG	328
QY	181	AAACTGAGACACTGAGAGATGCTGCTCTCCCTACCTTTCAATATAGATGCACAACCTAAG	240
Db	337	CACATTTGGTCAAT --- GAACCTTCCCTCCCTACCTTAATATATAGATGCACA --- TAGC	274
QY	241	GATAAAGACCTGAAACAAGGCACATCTCTCTGATTTCCGCGTGTACTTGTAAATGTTTGT	300
Db	273	AAACCCACCCCTGATGAGAGACACATCCTCTGGATTTCCGCGTGTCTGTTAAAGTTGTCT	214
QY	301	GTTTTGTGGGATGGTGTCTCTTTAAAACTAAGGAAAAAGAAAGAAAGCAAGCCGTGGC	360
Db	213	ATTTTGTGTGGATGGATGGTGTCTTTCTTAACCTAAGGAAAAAGAAAGAAAGCAAGCCGTGGC	154
QY	361	CCCTCTCATGATGTGAAACCATCAAAAGSGAGAGAAAGAGCAACAACGACCAACGAA	420
Db	153	CCCTCTCATGATGTGAAACCAACCAAAAGTGAAGAGAAAGAAAGTGAAGACCAACGAA	94
QY	421	AGAGTACCATTCACAGTACCTGAGAGATCTGATGTAAGCCCAAGTGTATTAACATTTTGAAG	480
Db	93	AGAGTACAGGTACCATGGAAGGGAAGATCTGATGTAAGCCCAAGTGTATTAACATTTTGAAG	34
QY	481	ACAGCCTCAGGCGCAAAAAGTACTACACA	509
Db	33	ACAGCCTCAGGCGCAACAGTACTACACA	5

DT 20-DEC-1999 (first entry)
 DE Canine B7-2 protein coding sequence.
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; canine;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 OS Canis familiaris.
 PN M09947558-A2.
 PD 23-SEP-1999.
 PE 19-MAR-1999; 99WO-US06187.
 PR 19-MAR-1998; 98US-0078765.
 PX 17-APR-1998; 98US-0062597.
 PA (HESKA -) HESKA CORP.
 PI Sim G, Yang S, Sellins KS;
 XX WPI: 1999-571822/48.
 DR P-PDB; AAY41076.
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases
 PS Claim 1; Page 102-103; 148pp; English.
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritic and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 SO Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other:
 Query Match 72.7%; Score 369.8; DB 20; Length 987;
 Best Local Similarity 85.7%; Pred. No. 6e-102;
 Matches 436; Conservative 0; Mismatches 67; Indels 6; Gaps 2
 QY 1 ATCAAGGTTACCCAGAACCCTAAGAGATGTATTTCAGCTTAACACTGAGAATTCACCT 60
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 481 ATCAAGGTTACCCAGAACCCTAAGAGATGTATTTCAGCTTAACAAACCCAGAAITTCACCT 540
 QY 61 ACTAGTAGTATGATACGTCTATGAAGAAATCTCAAATTAATGTACAACAATGTACAACGTT 120
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 541 ACTAGTAGTATGATACGTCTATGAAGAAATCTCAAATTAATGTACAACAATGTACAACGTT 600
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTCGAAGCACACAATGTAGCGCTTTTGTGCCCTG 180
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 601 TCTATCAGCTTGCTCTTCTCATGTCCTGGAAGACAAGTAATGATGCATCTTGTCGCTG 660
 QY 181 AACGCGAGACACTGGAATGCTGCTTCCTTCACTTTCAATAATAGATGACACACCTAAG 240
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 661 CAACCTGGAGTCAMT--GAAAGCTTCCCCTCCACCTTAATAATATGATGACACAA--TACG 714
 QY 241 GATAAAGACCTGGAACAAGGCGACCTCCGTCGATTTGGGGGCTGACTGTAATGTTTGT 300
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 715 AAACCCACCCCTGATGGAGAACACATCTCTGGAATGGGGCTCTCTGTAAATGTTGGTC 774
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 301 GTTTTTGTGGAGATGCTCTTTTAAACACTAAAGAAAAGGAAGAGACAGCGCTGCG 360
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 775 ATTGTGTGGAGATGCTTCTTTTAAACACTAAAGAAAAGGAAGAAAGACAGCGCTGCG 834
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 361 CCTCTCATGAATGTGAACCATCAAAAGGAGAGAAAAAGAGACCAACAGACCAACGAA 420
 Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

[illegible]

DB 726 AACTGAGACACTGAGATGCTGCTCCTACCTTTCAATATAGATGCAACAACCTAAG 785
OY 241 GATTAAGACCCCTGAACAAGGCGACACTGCTGATGCGGCTGACTGTAATGTTGTT 300
DB 786 GATTAAGACCCCTGAACAAGGCGACACTGCTGATGCGGCTGACTGTAATGTTGTT 845
OY 301 GTTTTGTGGAGTGTCTCTTTAAACACTAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
DB 846 GTTTTGTGGAGTGTCTCTTTAAACACTAAGAAAGAAAGAAAGAAAGAAAGAAAG 905
OY 361 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 420
DB 906 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 965
OY 421 AGAGTACCATACACGACTGAGAGATCTGATGAGAGCCAGTGTATTAACATTTGAAG 480
DB 966 AGAGTACCATACACGACTGAGAGATCTGATGAGAGCCAGTGTATTAACATTTGAAG 1025
OY 481 ACAGCCTCAGGCGACAAAGT 501
DB 1026 ACAGCCTCAGGCGACAAAGT 1046

RESULT 8
AA234785
ID AA234785 standard; cDNA; 1080 BP.
AC AA234785;
XX
DT 15-FEB-2000 (first entry)
XX
DE Cat CD86 (B7-2) cDNA.
XX
KM CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;
KM FIV; feline leukaemia virus; feline infectious peritonitis virus;
KM feline parvovirus; feline calicivirus; feline reovirus-3;
KM feline rotavirus; feline coronavirus; feline syncytial virus;
KM feline sarcoma virus; feline herpesvirus; feline boron disease;
KM rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;
KM parasite; autoimmune disease; transplant rejection; therapy; ss.
XX
OS Fells domesticus.
XX
FH Key Location/Qualifiers
FT CDS 63..1055
FT /*tag= a
XX
XX WO9957271-A2.
XX
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09502.
XX
XX 01-MAY-1999; 98US-0071699.
XX
XX (TEXA) TEXAS A & M SYSTEM.
XX
XX PA
XX PI Collison EM, Hash SM, Choi I;
DR WPI: 2000-052972/04.
XX P-PSDB; AAY32278.
XX
XX Novel feline proteins used to produce feline vaccines which prevent
PT infectious disease or to promote growth in homologous or heterologous
XX species -
XX
XX Claim 6; Fig 3A; 186pp; English.
XX
XX This is the nucleotide sequence of cDNA encoding feline CD86
CC (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
CC peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
CC comprising nucleic acid encoding feline CD86 ligand or feline
CC soluble CD80 ligand is designated PSI-2#19-2/011298 (ATCC 209821).

CC The coexpression of CD86 with the costimulatory molecules CD28 (see
CC AA32279) and a tumour antigen or an antigen from a pathogenic
CC organism has the ability to activate or enhance activation of
CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AA32280) has
CC the ability to regulate activation of T-lymphocytes. The invention
CC provides isolated nucleic acids encoding feline CD86 ligand,
CC feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
CC (CD152) receptor, as well as vectors comprising the nucleic acids,
CC and polypeptides encoded by the nucleic acids. It also provides
CC further comprising immunogens derived from pathogens, especially
CC feline immunodeficiency virus (FIV), feline leukaemia virus,
CC feline infectious peritonitis virus, feline parvovirus, feline
CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
CC herpesvirus, feline syncytial virus, rabies virus, chlamydia,
CC Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
CC pathogen, or parasite (all claimed). Vaccines capable of
CC enhancing an immune response, and vaccines capable of suppressing
CC an immune response (suitable for treating an autoimmune disease
CC or tissue or organ transplant rejection) are claimed. The
CC nucleic acids may be used for gene therapy or antisense therapy
CC protocols.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
Query Match 97.5%; Score 496.2; DB 21; Length 1080;
Best Local Similarity 99.4%; Pred. No. 2.9e-140;
Matches 498; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 ATACAGGTTACCCGAGAACCTAAGAGATGATTTTACGCTAAACAGTGAATTCAC 60
DB 546 ATACAGGTTACCCGAGAACCTAAGAGATGATTTTACGCTAAACAGTGAATTCAC 605
OY 61 ACTAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 606 ACTAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
OY 121 TCTATCAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 666 TCTATCAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 725
OY 181 AACTGAGAGACAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 726 AACTGAGAGACAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785
OY 241 GATTAAGACCCCTGAACAAGGCGACACTGCTGATGAGAGAGAGAGAGAGAGAGAG 300
DB 786 GATTAAGACCCCTGAACAAGGCGACACTGCTGATGAGAGAGAGAGAGAGAGAGAG 845
OY 301 GTTTTGTGGAGTGTCTCTTTAAACACTAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
DB 846 GTTTTGTGGAGTGTCTCTTTAAACACTAAGAAAGAAAGAAAGAAAGAAAGAAAG 905
OY 361 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 420
DB 906 CCTCTCATGATGTGAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 965
OY 421 AGAGTACCATACACGACTGAGAGATCTGATGAGAGCCAGTGTATTAACATTTGAAG 480
DB 966 AGAGTACCATACACGACTGAGAGATCTGATGAGAGCCAGTGTATTAACATTTGAAG 1025
OY 481 ACAGCCTCAGGCGACAAAGT 501
DB 1026 ACAGCCTCAGGCGACAAAGT 1046

RESULT 9
AA227915
ID AA227915 standard; DNA; 987 BP.
XX
XX AA227915;
AC
XX

DT	28-FEB-2000	(first entry)
XX		
DE	Feline CD86 (B7-2) cDNA.	
XX		
KM	CD86; B7-2; feline; cat; recombinant virus; vaccine;	
XX	immunomodulator; tumour; cancer; therapy; ss.	
XX		
CS	Felis domesticus.	
XX		
FM	Key	Location/Qualifiers
FT	CDS	63..1052
XX		/*tag- a
PN	W0957295-A1.	
XX		
PD	11-NOV-1999.	
XX		
PF	30-APR-1999;	99MO-US09504.
XX		
PR	01-MAY-1998;	98US-0071711.
XX		
PA	(SCHE) SCHERING-PLOUGH LTD.	
XX	(SCHE) SCHERING-PLOUGH VETERINARY CORP.	
XX		
PI	Winslow BJ, Cochran MD;	
XX		
DR	WPI: 2000-062155/05.	
XX	P-PSDB: AAY32285.	
PT	Novel recombinant virus useful as immunomodulators, particularly in	
PT	vaccines -	
XX		
PS	Disclosure; Fig 3a; 230pp; English.	
XX		
CC	This is the nucleotide sequence of cDNA coding for feline CD86	
CC	(B7-2). The cDNA was isolated from feline peripheral blood	
CC	mononuclear cell cDNA by PCR. Manipulating the expression of CD28	
CC	or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)	
CC	regulates T cell proliferation and cytokine release. The invention	
CC	relates to a recombinant virus that contains at least one foreign	
CC	nucleic acid, inserted into a nonessential genomic region, that	
CC	encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their	
CC	immunogenic fragments, and is expressed when the recombinant virus	
CC	is introduced into a suitable host. The invention also provides:	
CC	a recombinant virus further comprising a foreign nucleic acid	
CC	encoding an immunogen derived from a feline pathogen; recombinant	
CC	viruses capable of enhancing an immune response to protect against	
CC	disease; recombinant viruses expressing antisense sequences,	
CC	capable of suppressing an immune response in a feline, e.g. for	
CC	treatment of autoimmune disease or transplant rejection; and	
CC	recombinant viruses expressing DNA encoding CD80 and/or CD86 used	
CC	to reduce or eliminate a tumour in cats.	
XX		
SO	Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;	
XX		
Query Match	97.5%; Score 496.2; DB 21; Length 1080;	
Best Local Similarity	99.4%; Pred. No. 2,9e-140;	
Matches 499; Conservative	0; Mismatches 3; Indels 0; Gaps	0;
OY	1 ATACAGGTTACCCAGACACCTAAGAGATGATATTTTCAGCTAAACACTGAGAAATTCACCT	60
DB	546 ATACAGGTTACCCAGACACCTAAGAGATGATATTTTCAGCTAAACACTGAGAAATTCACCT	605
OY	61 ACTAGATGATGATCTGTCATGAAGAATCTCAAAATATATGACAGAGAACTGTCAACGTT	120
DB	606 ACTAGATGATGATCTGTCATGAAGAATCTCAAAATATATGACAGAGAACTGTCAACGTT	665
OY	121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAGCACAACAATGTGAGCGCTTTTGTGCCCTG	180
DB	666 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAGCACAACAATGTGAGCGCTTTTGTGCCCTG	725
OY	181 AATGTGAGACATGTGAGATGCTGCTCTCCACTTTCATATATAGATGCAACAACCTAAG	240

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QY 61 ACTAATGATGATCTGTCATGAGAAATCTCAAAATATGTCAGACACTGTACAACTGTT 120
DB 453 ACTAAGATGATGATCTGTCATGAGAAATCTCAAAATATGTCAGACACTGTACAACTGTT 394
QY 121 TCTATGAGCTTGGCTTTTTCAGTCCCGAAGACACAAATGTAGGCTCTTTTGTGCCCTG 180
DB 393 TCTATGAGCTTGGCTTTTTCAGTCCCGAAGACACAAATGTAGGCTCTTTTGTGCCCTG 334
QY 181 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATTAATATGATGCACAACTTAA 240
DB 333 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATTAATATGATGCACAACTTAA 274
QY 241 GATTAAGACCTTGAACAAAGGCCACTTCTCTGATTTCCGCTCTTACTTGTAAATGTTTGT 300
DB 273 GATTAAGACCTTGAACAAAGGCCACTTCTCTGATTTCCGCTCTTACTTGTAAATGTTTGT 214
QY 301 GTTTTGTGAGATGGTGCTCTTAAACATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
DB 213 GTTTTGTGAGATGGTGCTCTTAAACATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 154
QY 361 CCTCTCATGATGATGTAAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 420
DB 153 CCTCTCATGATGATGTAAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAA 94
QY 421 AGAGTACCATACCTGCTGATGAGATCTGATGAAGCCCACTGTATTAACTTTTGAAG 480
DB 93 AGAGTACCATACCTGCTGATGAGATCTGATGAAGCCCACTGTATTAACTTTTGAAG 34
QY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
DB 33 ACAGCCTCAGGCGACAAAGTACTACACA 5

RESULT 5
AAZ27929
ID AAZ27929 standard; DNA; 2830 BP.
XX
AC AAZ27929;
XX
DT 20-DEC-1999 (first entry)
XX
DE Feline B7-2 protein encoding DNA.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
P-PSDB; AMV41079.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g., autoimmune and atopic diseases
XX
PS Claim 1; Page 116-119; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
```

```
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other:
Query Match 100.0%; Score 509; DB 20; Length 2830;
Best Local Similarity 100.0%; Pred. No. 5,9e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATACAGGTTACCCAGACCTTACAGATGATTTTTCAGCTTAACTGAGAAATTCACCT 60
DB 662 ATACAGGTTACCCAGACCTTACAGATGATTTTTCAGCTTAACTGAGAAATTCACCT 721
QY 61 ACTAAGTATGATGATCTGTCATGAGAAATCTCAAAATATGTCAGACACTGTACAACTGTT 120
DB 722 ACTAAGTATGATGATCTGTCATGAGAAATCTCAAAATATGTCAGACACTGTACAACTGTT 781
QY 121 TCTATGAGCTTGGCTTTTTCAGTCCCGAAGACACAAATGTAGGCTCTTTTGTGCCCTG 180
DB 782 TCTATGAGCTTGGCTTTTTCAGTCCCGAAGACACAAATGTAGGCTCTTTTGTGCCCTG 841
QY 181 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATTAATATGATGCACAACTTAA 240
DB 842 AAACGTGAGACACTGAGATGCTGCTCTCCCTCTTTCATTAATATGATGCACAACTTAA 901
QY 241 GATTAAGACCTTGAACAAAGGCCACTTCTCTGATTTCCGCTCTTACTTGTAAATGTTTGT 300
DB 902 GATTAAGACCTTGAACAAAGGCCACTTCTCTGATTTCCGCTCTTACTTGTAAATGTTTGT 961
QY 301 GTTTTGTGAGATGGTGCTCTTAAACATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 360
DB 962 GTTTTGTGAGATGGTGCTCTTAAACATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1021
QY 361 CCTCTCATGATGATGTAAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 420
DB 1022 CCTCTCATGATGATGTAAACCATCAAAAGGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 1081
QY 421 AGAGTACCATACCTGCTGATGAGATCTGATGAAGCCCACTGTATTAACTTTTGAAG 480
DB 1082 AGAGTACCATACCTGCTGATGAGATCTGATGAAGCCCACTGTATTAACTTTTGAAG 1141
QY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
DB 1142 ACAGCCTCAGGCGACAAAGTACTACACA 1170

RESULT 6
AAZ27930/c
ID AAZ27930 standard; DNA; 2830 BP.
XX
AC AAZ27930;
XX
DT 20-DEC-1999 (first entry)
XX
DE Feline B7-2 gene complementary DNA sequence.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus.
XX
PN WO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
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RESULT 3
AA227931
ID AA227931 standard; DNA: 996 BP.
XX
XX AA227931;
AC
XX 20-DEC-1999 (first entry)
DT
XX
XX Feline B7-2 protein coding sequence.
DE
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
OS
XX WO9947558-A2.
PN
XX 23-SEP-1999.
PD
XX
XX 19-MAR-1999; 99WO-US06187.
PF
XX
XX 19-MAR-1998; 98US-0078765.
PR
XX 17-APR-1998; 98US-0062597.
PA
XX (HESK-) HESKA CORP.
XX
XX Slim G, Yang S, Sellins KS;
PI
XX WPI; 1999-571822/48.
DR
XX P-PSDB; AAY41079.
PT
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
PS
XX
XX Claim 1; Page 123-124; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other;
SQ
Query Match 100.0%; Score 509; DB 20; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.7e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATACAAGGTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTCAACT 60
DB 484 ATACAAGGTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTCAACT 543
OY 61 ACTAGTGTGATCTGATGATGAAGAAATCTCAAAATATGTCAGAGACTGTACAAAGCTT 120
DB 544 ACTAGTGTGATCTGATGATGAAGAAATCTCAAAATATGTCAGAGACTGTACAAAGCTT 603
OY 121 TCTATCAGCTGCTCTTTTTCAGTCCCTGAGACACAAATGTCAGGCTCTTTTGCCCTG 180
DB 604 TCTATCAGCTGCTCTTTTTCAGTCCCTGAGACACAAATGTCAGGCTCTTTTGCCCTG 663
OY 181 AAACGTGAGACACGTGAGATGCTGCTCCCTACCTTTCAATATATGATGACCAACCTTAAG 240
DB 664 AAACGTGAGACACGTGAGATGCTGCTCCCTACCTTTCAATATATGATGACCAACCTTAAG 723
OY 241 GATTAAGACCCGAGAACAGGCCACTTCCTGGATTTGGGCTGCTGATATGTTTGT 300
DB 724 GATTAAGACCCGAGAACAGGCCACTTCCTGGATTTGGGCTGCTGATATGTTTGT 783
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OY 301 GTTTTGTGGATGCTGCTTTTAAACACTAAGGAAAGAGAGAGAGCCCTGGC 360
DB 784 GTTTTGTGGATGCTGCTTTTAAACACTAAGGAAAGAGAGAGAGCCCTGGC 843
OY 361 CCTCTCATGATGTGTAACCATCAAAAGGAGAGAAAAAGAGCAACAGCCAAAGCA 420
DB 844 CCTCTCATGAAATGTGAACCATCAAAAGGAGAGAAAAAGAGCAACAGCCAAAGCA 903
OY 421 AGAGTCCATACACGCTACCTGAGAGATCTGATGAAGCCAGCTATTTAACATTTTGAAG 480
DB 904 AGAGTCCATACACGCTACCTGAGAGATCTGATGAAGCCAGCTATTTAACATTTTGAAG 963
OY 481 ACAGCCTCAGGGGACAAAAGTACTACACA 509
DB 964 ACAGCCTCAGGGGACAAAAGTACTACACA 992
RESULT 4
AA27932/C
ID AA27932 standard; DNA: 996 BP.
XX
XX AA27932;
AC
XX 20-DEC-1999 (first entry)
DT
XX
XX Complementary strand of feline B7-2 coding sequence.
DE
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Felis catus.
OS
XX WO9947558-A2.
PN
XX
XX 23-SEP-1999.
PD
XX
XX 19-MAR-1999; 99WO-US06187.
PF
XX
XX 19-MAR-1998; 98US-0078765.
PR
XX 17-APR-1998; 98US-0062597.
PA
XX (HESK-) HESKA CORP.
XX
XX Slim G, Yang S, Sellins KS;
PI
XX WPI; 1999-571822/48.
DR
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
PS
XX
XX Claim 1; Page 124-125; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;
SQ
Query Match 100.0%; Score 509; DB 20; Length 996;
Best Local Similarity 100.0%; Pred. No. 3.7e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATACAAGGTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTCAACT 60
DB 513 ATACAAGGTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTAAACACTGAGAAATTCAACT 454
```

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 125-126; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 509 BP; 170 A; 109 C; 106 G; 124 T; 0 other;
XX
Query Match 100.0%; Score 509; DB 20; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ATACAAGGTTACCCAGAACCTAAGAGAGATATTTTCAGTAACACTGAGATTTCAACT 60
DB 1 ATACAAGGTTACCCAGAACCTAAGAGAGATATTTTCAGTAACACTGAGATTTCAACT 60
OY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACAGCTT 120
DB 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACAGCTT 120
OY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACATGTGAGCGTCTTTTGCCCTG 180
DB 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACATGTGAGCGTCTTTTGCCCTG 180
OY 181 AAACCTGGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACAACTAAG 240
DB 181 AAACCTGGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACAACTAAG 240
OY 241 GATAAAGCCCTGGAACAGGCGACTCTCTGATGCGGCTGTACTGTATATGTTGTT 300
DB 241 GATAAAGCCCTGGAACAGGCGACTCTCTGATGCGGCTGTACTGTATATGTTGTT 300
OY 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGGAAAGAAAGAACACAGCTGCGC 360
DB 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGGAAAGAAAGAACACAGCTGCGC 360
OY 361 CCTCTCATGATGTGAAGCATCAAAAGGAGAGAAAGAGACAAACAGACCAAGAA 420
DB 361 CCTCTCATGATGTGAAGCATCAAAAGGAGAGAAAGAGACAAACAGACCAAGAA 420
OY 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGATATTAACATTTTGAAG 480
DB 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGATATTAACATTTTGAAG 480
OY 481 ACAGCCTCAGCGACAAAGTACTACACA 509
DB 481 ACAGCCTCAGCGACAAAGTACTACACA 509
XX
RESULT 2
AAZ27934/c
ID AAZ27934 standard; DNA; 509 BP.
XX
AC AAZ27934;
XX
DT 20-DEC-1999 (first entry)
XX
DE Feline B7-2 gene (larger fragment) complementary DNA sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Felis catus;

XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-0506187.
XX
XX 19-MAR-1998; 98US-0078765.
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPL; 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 127; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritic and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
SQ Sequence 509 BP; 124 A; 106 C; 109 G; 170 T; 0 other;
XX
Query Match 100.0%; Score 509; DB 20; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ATACAAGGTTACCCAGAACCTAAGAGAGATATTTTCAGTAACACTGAGATTTCAACT 60
DB 509 ATACAAGGTTACCCAGAACCTAAGAGAGATATTTTCAGTAACACTGAGATTTCAACT 60
OY 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACAGCTT 120
DB 61 ACTAGTATGATCTGTCATGAGAAATCTCAAAATTAATGTGACAGAACTGTACAGCTT 120
OY 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACATGTGAGCGTCTTTTGCCCTG 180
DB 121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAGACACATGTGAGCGTCTTTTGCCCTG 180
OY 181 AAACCTGGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACAACTAAG 240
DB 181 AAACCTGGAGACACTGAGATGCTGCTCCCTACCTTCAATATAGATGACAACTAAG 240
OY 241 GATAAAGCCCTGGAACAGGCGACTCTCTGATGCGGCTGTACTGTATATGTTGTT 300
DB 241 GATAAAGCCCTGGAACAGGCGACTCTCTGATGCGGCTGTACTGTATATGTTGTT 300
OY 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGGAAAGAAAGAACACAGCTGCGC 360
DB 301 GTTTTGTGGGATGCTGCTTTTAAACACTAAGGAAAGAAAGAACACAGCTGCGC 360
OY 361 CCTCTCATGATGTGAAGCATCAAAAGGAGAGAAAGAGACAAACAGACCAAGAA 420
DB 361 CCTCTCATGATGTGAAGCATCAAAAGGAGAGAAAGAGACAAACAGACCAAGAA 420
OY 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGATATTAACATTTTGAAG 480
DB 421 AGAGTACCATCCAGTACCTGAGAGATCTGATGAGCCCGATATTAACATTTTGAAG 480
OY 481 ACAGCCTCAGCGACAAAGTACTACACA 509
DB 481 ACAGCCTCAGCGACAAAGTACTACACA 509

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 : Search time 76.9499 Seconds
(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-30

Perfect score: 509
Sequence: 1 atacaaggtaccagaacc.....ggcgacaaagtracacaca 509

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802:.*
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2: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	100.0	509	20	AAZ27933
2	509	100.0	509	20	AAZ27934
3	509	100.0	996	20	AAZ27931
4	509	100.0	996	20	AAZ27932
5	509	100.0	2830	20	AAZ27929
6	509	100.0	2830	20	AAZ27930
7	496.2	97.5	1080	21	AAZ34838
8	496.2	97.5	1080	21	AAZ34785
9	369.8	72.7	987	20	AAZ27915

c	10	369.8	72.7	987	20	AAZ27916	Complementary stra
c	11	369.8	72.7	1897	20	AAZ27913	Canine B7-2 protei
c	12	369.8	72.7	1897	20	AAZ27914	Canine B7-2 gene c
c	13	268.8	52.8	1050	21	AAA49661	Pig costimulatory
c	14	227.2	44.6	359	20	AAZ27935	Feline B7-2 protei
c	15	227.2	44.6	359	20	AAZ27936	Feline B7-2 gene (
c	16	212.6	41.8	972	20	AAV83208	B7-2 cDNA. Homo s
c	17	212.6	41.8	972	24	AAZ25510	Human co-stimulat
c	18	212.6	41.8	1120	16	AAO81351	Human B lymphocyte
c	19	212.6	41.8	1120	18	AAV49181	Human B lymphocyte
c	20	212.6	41.8	1120	20	AAV55784	Human B7-2 antigen
c	21	212.6	41.8	1120	21	AAV55784	Human B lymphocyte
c	22	212.6	41.8	1120	21	AAV55784	Human B7-2 cDNA.
c	23	212.6	41.8	1428	16	AAO85873	B70 type B antigen
c	24	212.6	41.8	2205	22	AAH72616	Human cervical can
c	25	169.6	33.3	840	20	AAZ27923	Complementary stra
c	26	169.6	33.3	840	20	AAZ27924	Complementary stra
c	27	169.6	33.3	1795	20	AAZ27921	Canine B7-25 prote
c	28	169.6	33.3	1795	20	AAZ27922	Canine B7-25 gene
c	29	110	21.6	306	18	AAV49198	Human B lymphocyte
c	30	110	21.6	306	21	AAV49198	Human B lymphocyte
c	31	110	21.6	738	20	AAV80293	Human B7-2 constan
c	32	110	21.6	738	22	AAV89731	Human B7-2 extrace
c	33	110	21.6	764	18	AAV62939	Nucleotide sequenc
c	34	110	21.6	831	19	AAV03230	Chimeric human/por
c	35	99	19.4	210	16	AAV01038	DNA encoding CD86
c	36	77.2	15.2	1151	20	AAV55785	Human B7-2 exon 5.
c	37	77.2	15.2	1151	20	AAV55785	Human B7-2 antigen
c	38	77.2	15.2	1163	16	AAO81366	Mouse B lymphocyte
c	39	77.2	15.2	1163	18	AAV49182	Mouse B lymphocyte
c	40	77.2	15.2	1163	21	AAV49182	Mouse B lymphocyte
c	41	66	13.0	942	19	AAV01046	Mouse B7-2 exons m
c	42	66	13.0	942	19	AAV01046	Kat CD86 coding se
c	43	40	7.9	593	20	AAH68957	Human cervical can
c	44	36.6	7.2	1030	22	AAV20338	Borrelia burgdorfe
c	45	36.6	7.2	188	22	AAH71823	Human cervical can
c	46	36.6	7.2	146	22	AAV74416	Angiogenesis prote

ALIGNMENTS

RESULT 1	AAZ27933	standard; DNA; 509 BP.
ID	AAZ27933	standard; DNA; 509 BP.
AC	AAZ27933;	
XX		
XX		
DT	20-DEC-1999	(first entry)
XX		
DE	Feline B7-2 protein (larger fragment) encoding DNA.	
XX		
XX		
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;	
KW	allergic reaction; infectious disease; tumor development; feline;	
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.	
OS	Felis catus.	
XX		
PN	WO947558-A2.	
XX		
PD	23-SEP-1999.	
XX		
PF	19-MAR-1999;	99MO-US06187.
XX		
PR	19-MAR-1998;	98US-0078765.
XX		
PR	17-APR-1998;	98US-0062597.
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	Sim G, Yang S, Sellins KS;	
XX		
XX	WPI; 1999-571822/48.	
DR	P-PDB; AAY41080.	
XX		

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10296 row: k column: 20
High quality sequence stop: 283.
Location/Qualifiers

FEATURES

source

1..858

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4473739"
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/tissue_type="adenocarcinoma, cell line"
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/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 500 a 155 c 144 g 59 t

ORIGIN

Query Match

Best Local Similarity 8.0%; Score 40.8; DB 10; Length 858;
Matches 75; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 378 AACCATCAAAAGGAGAGAAAGAGAGCAACGAAAGGATGCCATACCAGCT 437
Db 464 AAACAACACGAGGAGGAGAGAAAGGAGAAAGCAAGCAAGCAACACACCA 523
QY 438 ACCTGAGAGATCTGATGAGCCAGTGTATTAACATTTTGAAGACAGCCTCGGAGCA 497
Db 524 AGCGGAAAAACCAACCAAAAAAGAGCAATTAACAAAGACAAAGCAACACCGAAGA 583
QY 498 AAGTACTACACA 509
Db 584 AAGAAAAAGGCA 595

RESULT 15

AA973397/c

LOCUS AA973397 378 bp mRNA linear EST 17-JUN-1998
DEFINITION o044a04.s1 NCI-CGAP_Lu5 Homo sapiens CDNA clone IMAGE:1569006 3',
similar to SW:CD86_HUMAN P42081 T LYMPHOCYTE ACTIVATION ANTIGEN

CD86 PRECURSOR ; mRNA sequence.
ACCESSION AA973397
VERSION AA973397.1 GI:3148577

KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 378)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 501 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham.

FEATURES

source

Location/Qualifiers
1..378

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/db_xref="taxon:9606"
/clone="IMAGE:1569006"
/clone_1ib="NCI-CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT773 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 113 a 65 c 90 g 110 t

ORIGIN

Query Match

Best Local Similarity 7.9%; Score 40.4; DB 9; Length 378;
Matches 60; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

QY 437 TACCTGAGAGATCTGATGACCCCAAGTGTATTAACATTTGAAGACAGCCTCAGCG 493
Db 375 TACCTGAAAGATCTGATGAGCCAGCGGTGTTTAAAGTTCGAGACATCTTCATGCG 316
QY 494 ACAAAAGTACTACA 507
Db 315 ACAAAAGTACTACA 302

Search completed: October 20, 2002, 04:30:10
Job time : 617.635 secs

Db	388	CCATTTACTGTAAGATGTGATGAAGCCACGGCTGTTTTTAAAGTTCACAACATCTTC	329
OY	489	AGGCACAATAAAGTACTACA	507
Db	328	ATCGACACAATAAGTATACA	310
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RESULT 12			
LOCUS	BG296224/c	503 bp	mRNA linear EST 21-FEB-2001
DEFINITION	602394048t1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4506082 5'		
ACCESSION	BG296224		
VERSION	BG296224.1 GI:13058645		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 503)		
JOURNAL	NIH-MGC http://mgi.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI0380 Row: 0 Column: 11 High quality sequence start: 2 High quality sequence stop: 465. Location/Qualifiers 1..503 /organism="Mus musculus" /db_xref="taxon:10090" /clone_image="IMAGE:4506082" /clone_lib="NIH_MGC_94" /tissue_type="retina" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC library."		
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FEATURES			
source			
<hr/>			
BASE COUNT			
ORIGIN	130 a	148 g	128 t
<hr/>			
Query Match 8.2% Score 41.6 DB 10; Length 503;			
Best Local Similarity 51.6%; Pred. No. 10;			
Matches 95; Conservative 0; Mismatches 89; Indels 0; Gaps 0;			
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Db	482	TTTTTGTTTGTGTTTGTGTTTTTTTCTTTTACCTGGTTCTCTTAAAAACAAG	423
OY	335	GAAAAGAAGAGAAGCAGCCCTGCTCATGAATGTGAACCATCAAAAGGAGA	394
Db	422	GGAACAGGAAAAATTGATGACACACGTCATCTTAAGCTCAAACTAAAAACAGAAC	363
OY	395	GAAAAGAGACAAACAGACCACAAAGAAAGTACATACACGTAAGAGATGTGATG	454
Db	362	AAACAAAGAGAAACATTGGCCCCCACCCCAAGCAACAATATATTACATGCTTTGG	303
OY	455	AAGC 458	
Db	302	CAAC 299	
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RESULT 13			

AL513871/c	AL513871	1101 bp	mRNA	linear	EST 13-FEB-2001
DEFINITION	AL513871 LTR1.NFL006.PL2 Homo sapiens cDNA clone CLOB40022A07 3 prime, mRNA sequence.				
ACCESSION	AL513871				
VERSION	AL513871.1 GI:12777365				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1101)				
JOURNAL	Li, W.B., Gruber, C., Jesse, J. and Polayes, D. Full-length cDNA libraries and normalization unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers				
FEATURES	source	1..1101			
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="CLOB40022A07"				
	/clone_id="LTR1.NFL006.PL2"				
	/tissue_type="Placenta"				
	/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA was primed with a NotI-Cligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	162 a	33 c	248 g	323 t	335 others
ORIGIN					
Query Match	8.1%; Score 41; DB 9; Length 1101;				
Best Local Similarity	33.9%; Pred. No. 13;				
Matches	56; Conservative 44; Mismatches 65; Indels 0; Gaps 0;				
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Db	181 CCCCBKRRKKRRKKRRKBCBCKBKRRKKRRKKRRKKRRKKRRKKCCBKRAA	122			
OY	327 AACACTAAGGAAAAGAGAAGAACACACCGCCCTCTCATGATGTGAACCATCAA	386			
Db	121 AA	62			
OY	387 AAGGAGAGAAAAGAGAGCAACAGACCCAGCAAGAAAGATTACATA	431			
Db	61 AA	17			
RESULT 14	858 bp	mRNA	linear	EST 13-FEB-2001	
LOCUS	CG252809				
DEFINITION	602365337BP1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4473739 5', mRNA sequence.				
ACCESSION	CG252809				
VERSION	CG252809.1 GI:12762625				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 858)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D.				

	BASE COUNT	282 a	242 c	244 g	234 t
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	Best Local Similarity	69.1%;	Pred. No.	0.0015;	
	Matches	96; Conservative	0; Mismatches	37; Indels	6; Gaps
					1;
QY	13 CCAGAACCTAAGAAGATGATTATTTTACGTAAACACTGAGATCACTACTAGTAGTGAT	72			
Dd	564 CGAAACCTPAGAAGATGATTATTTCTGTATA-----CTATTTCACCTATGACNTGTGT	617			
OY	73 ACGTCATGAAGAAACCTCAAATATATGTGCACAGACTGTRCACAAGCTTTTATCACCTGG	132			
Dd	618 GATPACTGCCGATATCATCACAGATTATGTCCACAGAACTGTTCATGTATCCAAACAGCTTC	677			
QY	133 CCTTTTTCAATCCCTCGAAG 151				
Dd	678 TCTCTTCATTCCTCCGATG 696				
	RESULT 10				
	B1132458				
LOCUS	B1132458	486 bp	mRNA	linear	EST 01-SEP-2001
DEFINITION	AR03JAIILN05GALIS Porcine Lymph node CDNA library, Cot 5 Sus scrofa				
ACCESSION	CDNA, mRNA sequence.				
VERSION	B1132458				
KEYWORDS	B1132458.1 GI:15413744				
SOURCE	pig.				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
TITLE	1 (bases 1 to 486)				
JOURNAL	Rink,A.; Santischl,E.M. and Beattie,C.W. Amplified, Normalized CDNA Libraries from a Porcine Model of Orthopedic Implant Associated Staphylococcus aureus Infection Unpublished (2001) Contact: Rink A				
COMMENT	Department of Animal Biotechnology College of Agriculture, Biotechnology and Natural Resources, University of Nevada, Reno MS 202, FA 103, 1664 N Virginia St., Reno, NV 89557-0236, USA Tel.: 775 784 1705 Fax: 775 784 1375 Email: arlink@cabnr.unr.edu Tissues and cells are derived from a porcine model for implant-associated infection using 1000 ctu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cdna adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGACAGAG'. Location/Qualifiers 1..486 organism="Sus scrofa" strain="crossbred" db_xref="taxon:9823" clone_lib="Porcine lymph node CDNA library, Cot 5" tissue_type="Lymph node" cell_type="mixed" dev_stage="control, 5 month old castrated male" lab_host="SOLR" note="vector: pBSK; Site_1: Eco RI; Site_2: XhoI; Tissues: and cells are derived from a porcine model for implant-associated infection using 1000 ctu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cdna adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGACAGAG'."				
FEATURES					
SOURCE					
BASE COUNT	144 a	98 c	75 g	150 t	19 others
ORIGIN					
Query Match	10.8%; Score 54.8;	DB 10;	Length 486;		

[illegible]

source 1. 753
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5212648"
/clone_lib="NIH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC library."

BASE COUNT 227 a 166 c 156 g 204 t
ORIGIN

Query Match 16.5%; Score 84; DB 10; Length 753;
Best Local Similarity 81.8%; Pred. No. 1e-09; 25; Indels 2; Gaps 2;
Matches 121; Conservative 0; Mismatches 25; Indels 2; Gaps 2;

Db 1 ATACAGGTTCACCAAGCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCACCT 60
|||||
585 ATACACGGTTACCAAGACCTAAGAGATG-AGTGTTCAGTAAAGAACCAATTCACCT 643

QY 61 ACTAGTATGATCTGTC-ATGAAGAAATCTCAAAATATGTCAGACACTGTACACCT 119
|||||
644 ATCCAGTATGATCTGATTTATGTCAGAAATCTCAAGATATGTCACAGCTGTACAGCT 703

QY 120 TTCTATGAGCTTGCCTTTTTCAGTCCCT 147
|||||
Db 704 TTCCATCAGCTTGTCTGTTTCATTCCT 731

RESULT 8
A1750143/c 480 bp mRNA linear EST 22-JUN-1999
LOCUS A1750143
DEFINITION ac27h10.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2356387 3' similar to SW:CD86, HUMAN P42081 T LYMHOCYTE
ACTIVATION ANTIGEN CD86 PRECURSOR, mRNA sequence.
ACCESSION A1750143
VERSION A1750143.1 GI:5128407
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 480)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400p from G100
High quality sequence stop: 367.
Location/Qualifiers
1. 480
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2356387"
/clone_lib="Barstead aorta HPLRB6"

/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/note="Organ: aorta; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker. Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTACGAAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
[5' ATTTCGATCGAAC 3' and 5' GTTGGATCGG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barstead."

BASE COUNT 123 a 107 g 157 t
ORIGIN

Query Match 15.4%; Score 78.6; DB 9; Length 480;
Best Local Similarity 74.6%; Pred. No. 1.9e-08;
Matches 126; Conservative 0; Mismatches 39; Indels 4; Gaps 2;

QY 342 GAAGAAGACGACCTGGCCCTCTCATGATGTGAACCATCAAGGAGAGAAAGA 401
|||||
Db 475 GAAGAAGACGCGGCGCTCGCACTCTATAAATGTG-GACCAACAAATGAGAGGAGA 417

QY 402 GAGCAACGACGACCAAGAGATACCATCCAGCTGAGATCGATGAGAGCCCA 461
|||||
Db 416 GAGTGAACAGACCAAGAAAGAAAAAATCATATTACTGAAAGATGATGAGCCCA 357

QY 462 GTG--TATTACATTTGAGACAGACCTCAGCGCAAAAGTACTACA 507
|||||
Db 356 GCGGTGTTTAAAGTTCGAAAGCATCTTCATCGCAAAAGTATACA 308

RESULT 9
BF137460 1002 bp mRNA linear EST 24-OCT-2000
LOCUS BF137460
DEFINITION 601780644F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008635 5',
mRNA sequence.
ACCESSION BF137460
VERSION BF137460.1 GI:10976500
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1002)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
http://image.llnl.gov
Plate: L14M9243 row: h column: 12
High quality sequence stop: 663.
Location/Qualifiers
1. 1002
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:4008635"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; transgenic model MMT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 606.635 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-30

Perfect score: 509
Sequence: 1 atacaaggtaccagacc.....ggcgcacaaagtactacaca 509

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbta:*
2: em_estbhum:*
3: em_estlin:*
4: em_estlun:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	241.8	47.5	512	9	AA056905 EST224F P
C 2	121.4	23.9	496	9	AW516826 xq04h01.x
C 3	109.8	21.6	347	10	BG001664 RC4-GN006
C 4	108.8	21.4	543	10	BF064222 7357b02.x
C 5	102.2	20.1	570	9	AT093604 ou82b09.s
C 6	97.4	19.1	504	9	AA946810
C 7	84	16.5	753	10	BI906246 603063172
C 8	78.6	15.4	480	9	AT150143 at27h10.x
C 9	57.8	11.4	1002	10	BF137460 601780644
C 10	54.8	10.8	486	10	BI132458 AR03A11L
C 11	42.2	8.3	391	9	AT632116 l885b01.x
C 12	41.6	8.2	503	10	BG296224 602394048
C 13	41	8.1	1101	9	AL513871
C 14	40.8	8.0	858	10	BG252809 602365378
C 15	40.4	7.9	378	9	AA973397 o044a04.s
C 16	40.4	7.9	1657	10	BG181018 602329129
C 17	40.2	7.9	741	12	AZ175416 SP_0132_A

C 18	39.8	7.8	303	9	AT569637 t044g09.x
C 19	39.6	7.8	919	10	BF036274
C 20	39.2	7.7	629	12	AZ358039 1M0100G01
C 21	38.8	7.6	316	9	AL514579
C 22	38.8	7.6	1101	12	CNS0039V
C 23	38.6	7.6	1101	12	CNS04529
C 24	38	7.5	1101	12	CNS00D03
C 25	37.8	7.4	1074	12	CNS015JW
C 26	37.8	7.4	1754	10	BG422600 602447090
C 27	37.6	7.4	402	10	BI503030
C 28	37.6	7.4	553	10	BG285180 602409487
C 29	37.4	7.3	619	12	FR0004538
C 30	37.4	7.3	953	12	CNS006PF
C 31	37.2	7.3	464	9	AA304943
C 32	37.2	7.3	511	12	AZ245001
C 33	37.2	7.3	981	9	AL664130
C 34	37.2	7.3	386	10	BE921986 EST425755
C 35	37	7.3	512	12	AQ342188
C 36	37	7.3	679	10	BM406580
C 37	37	7.3	1072	12	AG186990
C 38	36.8	7.2	298	9	AM655358
C 39	36.8	7.2	327	10	BI294883
C 40	36.8	7.2	357	9	BE120284
C 41	36.8	7.2	382	10	H35362
C 42	36.8	7.2	430	10	BG669718
C 43	36.8	7.2	441	9	AW50155
C 44	36.8	7.2	502	10	BF564120
C 45	36.8	7.2	790	3	BI644890

ALIGNMENTS

RESULT 1
AA056905/c 512 bp mRNA linear EST 18-SEP-1996
DEFINITION
EST224F Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)
Sus scrofa cDNA clone SPL224 forward similar to U25259 CT1A4
counter-receptor , human, mRNA sequence.

ACCESSION
AA056905
VERSION
AA056905.1 GI:1549545
KEYWORDS
EST.
SOURCE
Sus scrofa
ORGANISM
pig.
REFERENCE
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS
Tuggle C.K., Mahls S. and Schmitz C.
TITLE
Expressed Sequence Tags from Pig Spleen
JOURNAL
Unpublished (1996)
CONTACT
Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: ktuggle@iastate.edu
PCR PRIMERS
FORWARD: TGCGCAGACTCTG
BACKWARD: GACCGCGCTCAGT
Insert Length: 950 Std Error: 50.00
Seq primer: TGCGCAGACTCTG.
FEATURES
source
1..512
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="SPL224"
/clone_lib="Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)"
/tissue_type="spleen"
/dev_stage="adult"
/note="Oligo (dT) primed"

BASE COUNT 125 a 106 c 114 g 163 t 4 others

Db 484 ATACAGGGTTACCCAGAACCTAGAGATGATGTTTTGCTAAGACCAAGATTCAACT 543
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGACAGAACTGTACAGCTT 120
Db 544 ATCGAGTATGATGATGATGAGAAATCTCAAGATATGACAGAACTGTACAGCTT 603
QY 121 TCTATCAGCTTCCCTTTTCAGTCCCTGAG---CACACAATGTGAGCGCTTTTGCC 177
Db 604 TCCATCAGCTTCTGTTTTCATCTCCATGATGTACAGCAATATGACCAATCTCTGTATT 663
QY 178 CTGAAGTGTGAGACAGCTGAGATGCTGCTCCCTACCTTTCAATATGATGACAACT 237
Db 664 CTGGAAGTGTGAGACAGCTGAGATGCTGCTCCCTACCTTTCAATGATGACAACT 714
QY 238 AAGGATTAAGACCTTGACAAAGCCACTTCTCTGTGATTTGGCGCTGTCTGTATGTTT 297
Db 715 GAGGACCTGTACGCTCCCGACAGACCAATCTCTGATTTACAGCTGTACCAACACTT 774
QY 298 GTTGTTTTTTGGGATGCTGCTTTTAAACACTAAGAAAGGAGAAAGACAGCCT 357
Db 775 ATTATATGTGTGATGCTTTTCTGTCTATGTCATGAAATGGAAGAGAGGCGCT 834
QY 358 GGCCCTCTCATGATGTAACCAATCAAAAGGAGAGAGAAAGACCAACAGCCAC 417
Db 835 CGCACTCTTATTAATGTGAACCAACCAATGAGAGGAGAAAGAGACAGCCAC 894
QY 418 GAAAGATGACCTTACAGCTGCTGAGATGCTGATGAGCGCCAGTG---TATTAACATT 474
Db 895 AAGAGAGAAATCAATATCTGAAAGATCTGATGAGCGCCAGTG---TATTAACATT 954
QY 475 TTGAAGACAGCTCAGCGACCAAAAGTACTACA 507
Db 955 TCGAAGACATCTTTCATGCGACAAAGTGATACA 987

RESULT 13

HUMB72A 1112 bp mRNA linear PRI 31-DEC-1994
LOCUS Human CTIA4 counter-receptor (B7-2) mRNA, complete cds.
DEFINITION L25259
ACCESSION L25259.1 GI:416368
VERSION CTIA4 counter-receptor.
KEYWORDS CTIA4 counter-receptor.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1112)
Freeman,G.J., Grubben,J.G., Bousiotsis,V.A., Ng,J.W., Restivo,V.A., Jr., Lombard,L.A., Gray,G.S. and Nadler,L.M.
Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell proliferation [see comments]
JOURNAL Science 262 (5135), 909-911 (1993)
MEDLINE 94053735
FEATURES
source
1..1112
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="B lymphocyte"
1..1112
/gene="B7-2"
107..1096
/gene="B7-2"
/codon_start=1
/product="CTIA4 counter-receptor"
/protein_id="AA58389.1"
/translation="MDPQCTGLSNIILFVNAFLISGAAPLIQAVENETADLPQCPAN
SONSLSELVFMQDQENILVNEYLGKEDSVSHSKMGRTSDSDSWLRLNLDI
KDKGLYOCIIHKRPETGRIHOMNSELVANSOPEIYVLSINTENVYINTCSSI
HGYPEPKMSVILRTKNTIYDGIOMKSDONTEIVDYSISLVSFDPVSNMTIC
ILFDKTRLLSPSIELEDDPPDPDPIPTALIPYIICVMPCLIMKKKKRP
RNSYKGTNINIERESEDOTKKREKIHIPERSDEARVFKSKTSKDSKSDICP"
sig_peptide 107..175

mat_peptide /gene="B7-2"
176..1093
/gene="B7-2"
polya_site /product="CTIA4 counter-receptor"
1112
/gene="B7-2"
BASE COUNT 346 a 237 g 230 g 299 t
ORIGIN
Query Match 41.8%; Score 212.6; DB 9; Length 1112;
Best Local Similarity 69.0%; Pred. No. 5.5e-49;
Matches 354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;
QY 1 ATCAAGGTATACCCAGAACTAAGAGATGATTTTTCAGCTTAACTAAGATCAACT 60
Db 584 ATACAGCTTATCCAGAACCTAAGAGATGATGTTTGTCTAAGAACCAAGATTCAACT 643
QY 61 ACTAAGTATGATCTGTCATGAGAAATCTCAAAATATGATGACAGAACTGTACAGCTT 120
Db 644 ATCAGATGATGATGATATGAGAAATCTCAAGATATGTCAGAGAACTGTACAGCTT 703
QY 121 TCTATCAGCTTCCCTTTTCAGTCCCTGAG---CACACAATGTGAGCGCTTTTGCC 177
Db 704 TCCATCAGCTTCTGTTTTCATCTCCATGATGTACAGCAATATGACCAATCTGTATT 763
QY 178 CTGAAGTGTGAGACAGCTGAGATGCTGCTCCCTACCTTTCAATATGATGACAACT 237
Db 764 CTGGAAGTGTGAGACAGCTGAGATGCTGCTCCCTACCTTTCAATATGATGACAACT 297
QY 238 AAGGATTAAGACCTTGACAAAGCCACTTCTCTGTGATTTGGCGCTGTCTGTATGTTT 297
Db 815 GAGGACCTGTACGCTCCCGACAGACCAATCTCTGATTTACAGCTGTACTTCCACAGTT 874
QY 298 GTTGTTTTTTGGGATGCTGCTTTTAAACACTAAGAAAGGAGAAAGACAGCCT 357
Db 875 ATTATATGTGTGATGCTTTTCTGTCTATGTCATGAAATGGAAGAGAAAGCGCCT 934
QY 358 GGCCCTCTCATGATGTAACCAATCAAAAGGAGAGAGAAAGACCAACAGCCAC 417
Db 935 CGCACTCTTATTAATGTGAACCAACCAATGAGAGGAGAGATGAGTGAACAGCAAG 994
QY 418 GAAAGATGACCTTACAGCTGCTGAGATGCTGATGAGCGCCAGTG---TATTAACATT 474
Db 995 AAGAGAGAAATCAATATCTGAAAGATCTGATGAGCGCCAGTG---TATTAACATT 1054
QY 475 TTGAAGACAGCTCAGCGACCAAAAGTACTACA 507
Db 1055 TCGAAGACATCTTTCATGCGACAAAGTGATACA 1087

RESULT 14

AR030780 1120 bp DNA linear PAT 29-SEP-1999
LOCUS AR030780
DEFINITION Sequence 1 from patent US 5861310.
ACCESSION AR030780
VERSION AR030780.1 GI:5943994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1120)
Freeman,G.J., Nadler,L.M. and Gray,G.S.
Tumor cells modified to express B7-2 with increased immunogenicity
and uses therefor
JOURNAL Patent: US 5861310-A 1 19-JAN-1999;
MEDLINE
FEATURES
source
1..1120
/organism="unknown"
/location/Qualifiers
BASE COUNT 354 a 237 c 230 g 299 t
ORIGIN
Query Match 41.8%; Score 212.6; DB 6; Length 1120;
Best Local Similarity 69.0%; Pred. No. 5.5e-49;

LOCUS	ARI47736	1002 bp	DNA	Linear	PAT 08-AUG-2001
DEFINITION	Sequence 33 from patent US 6225042.				
ACCESSION	ARI47736				
VERSION	ARI47736.1	GI:15111826			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1002)				
AUTHORS	Cal,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.				
TITLE	Antigen presenting system and methods for activation of T-cells				
NOTE	Patent: US 6225042-A 33 01-MAY-2001;				
FEATURES	Location/Qualifiers				
source	1..1002				
	/organism="unknown"				
BASE COUNT	309 a 215 c 203 g 275 t				
ORIGIN					
Query Match	41.8%;	Score 212.6;	DB 6;	Length 1002;	
Best Local Similarity	69.0%;	Pred. No. 5.5e-49;			
Matches 354;	Conservative 0;	Mismatches 144;	Indels 15;	Gaps 4;	
1	ATACGAAGTTACCCAGAACCTAAGAGATGTTTTCACCTAAACAGTACAGATTCACCT	60			
484	ATACACGGTTACCCAGAACCTAAGAGATGATGTTTTCGTAAAGAACCAAGATTCACCT	543			
61	ACTAAGATGATACTGCTCATAGAAATCTCAAAATTAATGTGACAGAACTGTACACGTT	120			
544	ATCGATGTATGATGATATTATATGACAAATCTCAAGATTAATGTACAGAACTGTACACGTT	603			
121	TCTATCAGTTCGCCCTTTTTCAGTCCCTGAG---CACACATGTGAGCGCTCTTTGTGCC	177			
604	TCCATCAGCTGTCTGTTTCATTTCCCTGATGTTACGAGCAATATGATCACCATCTTCGTATT	663			
178	CTGAACATGAGACACTGGAGATGCTGCTCCCTACCTTCATATATGATGCACACCT	237			
664	CTGGAACCTGNA---AGACGGCGCTTTTATCTTACCTTCTCTATAG-----AGCTT	714			
238	AAGATTAAGACCTGGAACAAAGGCCACTTCTCTGATGTCGGCTGTACTGTGTAATGTTT	297			
715	GAGGACCTCTACGCCCTCCCCAGACCAACATTCCTGTGATTACAGCTGTACTTCCACAGTT	774			
298	GTTGTTTTTGGGATGGTGGCTTTTAAACACCTAAGAAAGGAAGAAGAAGAGAGCT	357			
775	ATTATATGTGATGATGTTTCTTCTTAATTCTATGGAATGGAGAAGAGAGCGGCT	834			
358	GGCCCTCTCATGATGTGAAACCATCAAAAGGAGAGAAAGAGAGCAACAGACCAAC	417			
835	CGCACTCTTTAATAATGTGGAACCAACCAATGGAGAGGAGAGAGTGAACAGACCAAG	894			
418	GAAGAAGTACCATTACCAGCTACTAGAGATCTGATGAAGCCCACTG---TATTACATT	474			
895	AAAAAGAAAAAATCATATACCTTAAGAAGATCTGATGGAAGCCACCGCTTTTAAAAAGT	954			
475	TTGAAGACAGGCTCAGGCGACAAAAGTACTACA	507			
955	TGGAAGACATCTTTCATGTGAGCAAAAGTATACA	987			
LOCUS	ARI59758	1002 bp	DNA	Linear	PAT 17-OCT-2001
DEFINITION	Sequence 33 from patent US 6251627.				
ACCESSION	ARI59758				
VERSION	ARI59758.1	GI:16222530			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1002)				
AUTHORS	Cal,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.				
TITLE	Antigen presenting system and methods for activation of T-cells				
NOTE	Patent: US 6251627-A 33 26-JUN-2001;				
JOURNAL					

FEATURES	Location/Qualifiers
SOURCE	1..1002 /organism="unknown"
BASE COUNT	309 a 215 c 203 g 275 t
ORIGIN	
Query Match	41.8%; Score 212.6; DB 6; Length 1002;
Best Local Similarity	69.0%; Pred. No. 5.5e-49;
Matches 354; Conservative	0; Mismatches 144; Indels 15; Gaps 4
QY	1 ATCAAGGTTACCCAGAACCTTAAGAGATGTAATTTTCACCTTAACACTGAGATTCACT 60
DB	484 ATACACGGTTACCCAGAACCTTAAGAGATGTAATTTTCACCTTAACACTGAGATTCACT 543
QY	61 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATTAATGTGACAGACTGACACGTT 120
DB	544 ATCGAGTATGATGATGTAATTTGCAAGAAATTCAGATTAATGTACACAGACTGACACGTT 603
QY	121 TCTATCAGCTTCCCTTTTTCAGTCCCTGAAG--CACACAATGTGAGCGCTTTTGTGCC 177
DB	604 TCCATCAGCTTGTCTGTTCATTCCTCGATGTTAGCAGCAATATGACATCTTCTATT 663
QY	178 CTGAAGCTGGAACACTGGAAGATGCTGCTCCCTCACTTCAATTAATGACACACT 237
DB	664 CTGGAAGCTGACA---AGCGCGGCTTTATCTTCACTTCTCTATA-----AGCTT 714
QY	238 AAGGATAAAGACCTTGAAACAGGCCACTTCCCTGTGATGCGGCTGTACTTGAATGTT 297
DB	715 GAGGACCTTCACCTCCGCCAGACACATTCCTTGATTAACAGCTGTACTTCCACAGTT 774
QY	298 GTTGTTTTGTGGGATGCTGCTCTTTTAAACACTTAAGAAAAAGAAAGACAGCCT 357
DB	775 ATTATATGTGATGATGTTTCTGTCTAATCTATGGAATGGAAGAAAGAGCGGCT 834
QY	358 GGCCCTCTCATGATGATGTAACCATCAAAAGGAGAGAAAGAGAGACCAACAGACCAAC 417
DB	835 CGCACTCTTAAATATGTTGGAACACACAAATGGAAGGGAAGGAGAGATGACAGACCAAG 894
QY	418 GAAAGATGACCTACACAGTACCTGAGAGATCTGATGAAGCCCACTG--TATTAACATT 474
DB	895 AAAAAGAAAAAATCCATATACCTAAAGATCTGATGAAGCCACAGCTGTTTTTAAAGT 954
QY	475 TTGAAGACAGCCTCAGGCGACAAAGTACTTACA 507
DB	955 TCGAAGACATCTTCAATGCGACAAAGTACTACA 987
RESULT 12	
ARI60450	1002 bp DNA linear PAT 17-OCT-2001
LOCUS	ARI60450
ACCESSION	Sequence 33 from patent US 6255073.
VERSION	ARI60450.1 GI:16224366
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1002)
AUTHORS	Cal,Z., Sprent,J., Brunmark,A., Jackson,M. and Peterson,P.A.
TITLE	Antigen presenting system and methods for activation of T-cells
JOURNAL	Patent: US 6255073-A 33 03-JUL-2001;
FEATURES	Location/Qualifiers
SOURCE	1..1002 /organism="unknown"
BASE COUNT	309 a 215 c 203 g 275 t
ORIGIN	
Query Match	41.8%; Score 212.6; DB 6; Length 1002;
Best Local Similarity	69.0%; Pred. No. 5.5e-49;
Matches 354; Conservative	0; Mismatches 144; Indels 15; Gaps 4;
QY	1 ATCAAGGTTACCCAGAACCTTAAGAGATGTAATTTTCAGCTTAACACTGAGATTCAACT 60

ORGANISM	Macaque mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
AUTHORS	1 (bases 1 to 1048) Villinger,F., Bostik,P., Mayne,A.E., King,C.L., Genain,C.P., Weiss,W.R. and Ansari,A.A.
TITLE	Cloning, sequencing, and homology analysis of nonhuman primate Fas/FasL ligand and co-stimulatory molecules
JOURNAL	Immunogenetics 53 (4), 315-328 (2001)
MEDLINE	21383618
PUBMED	11491535
REFERENCE	2 (bases 1 to 1048)
AUTHORS	Villinger,F.
TITLE	Direct Submission
JOURNAL	Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory University School of Medicine, Winship Cancer Institute, 1365B Clifton Rd, Atlanta, GA 30322, USA
FEATURES	Location/Qualifiers 1..1048
source	/organism="Macaca mulatta" /db_xref="taxon:9544" 19..68 19..990 /note="B7.2" /codon_start=1 /product="CD86 protein precursor" /protein_id="AAK37540.1" /db_xref="GI:13650012"
sig_peptide	
CDS	
BASE COUNT	324 a 230 c 205 g 289 t
ORIGIN	
Query Match	42.3%; Score 215.2; DB 9; Length 1048;
Best Local Similarity	69.3%; Pred. No. 1e-49;
Matches 356; Conservative	0; Mismatches 143; Indels 15; Gaps 4;
Dn	1 ATACAGGTTCCGCCGAACCTAAGAGATGTATTTCAGCTAACAGCAGAAATCAACT 60
Dn	478 ATACAGGTTCCGCCGAACCTAAGAGATGTATTTCAGCTAACAGCAGAAATCAACT 537
Dn	61 ACTAGTATGATACGTATGAGAAGAAATCTCAAATAATGTGACAGAACTGTACAAGTT 120
Dn	538 ATCGATGTGATGGTGTTTATGCAGAAATCTCAAGTAATGTGACAGAACTGTACAAGTT 597
Dn	121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAG--CACACAAATGTGAGCTCTTTTGTGCC 177
Dn	598 TCACATCAGCTTGCTGTTTCATTCCCTGATGTTTACGAGCAACATACCACTCTTCTGTGT 657
Dn	178 CTGAACATGAGACACTGGAGATGTCGTCCTCCCTACCTTCAATATGATGCACAACT 237
Dn	658 CTGGAAGTACGAAA---AGACACAGCTTTTATCTCTACACTTCTCTATG-----AGCTT 708
Dn	238 AAGATTAAGACCTGGAACAGGCACTTCTCTGAGTTGGGCTGTACTGTATATTTTT 297
Dn	709 GAGGACCTCTACCTCCGCCACAGCAACATCCCTTGATTAACAGCTGACTTCCAACAGTT 768
Dn	296 GTTGTATTTTGGGATGSGTGTCTTAAACACTAAGAAAAAGGAAGAAAGCAAGCT 357
Dn	769 ATTATATGTGTATGCTTCTGTCTAATTTCTATGGAATGGAAGAGAGAGAGAGCT 828
Dn	358 GGCCCCCTCATGAATGTGGAACCATCAAAAGGAGAGAAAGAGAGCAAGACCAAC 417
Dn	829 CCAACTCTTTAATAATGTGGAACCAACAAATGAGAGAGAGAGAGTAGTGAACAGACAAA 888
Dn	418 GAAGATGATCACTACCTACCTAGAGATCTGATGAAGGCCAGG---TATTACATT 474
Dn	889 AAAAGGAAAAAATTATATCTTACCTGAAGATCTGTGAGAGGCCCAATATGTTTAAAAGT 948

LOCUS	AX027005	972 bp	DNA	linear	PAT 16-SEP-2000
DEFINITION	Sequence 2 from Patent W00037102.				
ACCESSION	AX027005				
VERSION	AX027005.1	GI:10188040			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 972)				
AUTHORS	Rogers,N.J., Dorling,A. and Lechler,R.I.				
TITLE	Immunosuppression				
JOURNAL	Patent: WO 0037102-A 2 29-UN-2000; ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ; LECHLER ROBERT IAN (GB)				
FEATURES	source location/Qualifiers				
BASE COUNT	304 a 204 c 194 g 270 t				
ORIGIN					
Query Match	41.8%; Score 212.6; DB 6; Length 972;				
Best Local Similarity	69.0%; Pred. No. 5.5e-49;				
Matches	354; Conservative 0; Mismatches 144; Indels 15; Gaps 4;				
1	ATACAGGTTACCCAGAACCTAAGAGATGTAATTTTCACGTAACAACCTGAGAAATTCACACT	60			
2					
3	460 ATACAGCGTTACCCAGAACCTAAGAGAGATGTAATTTTCACGTAACAACCTGAGAAATTCACACT	519			
4	61 ACTAAGTATGATACGTCTCATGGAAGAAATCTCAAAATTAATGTGACAGCAACTGTACAAAGTT	120			
5	520 ATCGAGTATGATGCTATTTATGCGAAGAAATTCGAAGATTAATGTACACAGCAACTGTACAGCTT	579			
6	121 TCTATCAGCTTCCCTTTTTCAGTCCCTGAG--CACACAATGTGAGCGCTTTTGTGCC	177			
7					
8	580 TCCATCAGCTTCTGCTTTTCATTCCTCGATGTTACAGACAAATATGACCATCTTCTGCTATT	639			
9	178 CTGAACACTGGAACACTGGAAGATGCTGCTCTCCCTTACCTTTCAATATATGATGACACACT	237			
10					
11	640 CTGGAAGACTGACA--AGACGGCGCTTTTATTTTCACTTTCTCTATAA----AGCTT	690			
12	238 AAGGATTAAGACCTCTGAACAAAGGCCACTTCCTGATGTGGCGTGTACTTGTAAATGTTT	297			
13					
14	691 GAGGACCTTCACGCTCCGCCAGACCAACATTCCTTGATTCAGCTGTACTTCCAAACAGTT	750			
15	298 GTTGTTTTTTGTGGATGCTGCTTTTAAACACTAAGGAAAAAGGAAGAAGCAGCT	357			
16					
17	751 ATTATATGTGTATGGTGTCTTCTGCTAATTCTATGGAATGTGAAGAAAGGAGCGGCT	810			
18	358 GGGCCCTCTCATGATGTGTAACCATCAAAAGGAGAGAAAGAGAGCAACAGACCAAC	417			
19					
20	811 CCAACTCTTTATAAATGTTGGAACCAACAAATGGAAGGGAAGAGTGTAACAGACCAAG	870			
21	418 GAAAGAGTCCATACCACTACCTGAGAGATCTGATGAGAGCCAGT---TATTACATT	474			
22					
23	871 AAAAGGAAAAATTCATATACCTGGAATATCTGATGAGAGCCAGCGTGTTTTAAAGT	930			
24	475 TTGAAGACAGCCTCAGGCGAACAAGTACTACA	507			
25					
26	931 TCGAAGACATCTTCATGCGACAAAGTGTATACA	963			

JOURNAL Patent: WO 0037102-A 13 29-JUN-2000;
ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;
LECHLER ROBERT IAN (GB)
FEATURES Location/Qualifiers
source 1..994
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN
Query Match 52.8% ; Score 268.8 ; DB 6 ; Length 994 ;
Best Local Similarity 75.5% ; Pred. No. 9.2e-65 ;
Matches 391; Conservative 0; Mismatches 112; Indels 15; Gaps 4 ;
QY 1 ATACAAGTTACCCAGAACCTAAGAGATGATATTTTACCTAAGACCTGAGAAATCAACT 60
DB ACACAGAGCTACCCAGAACCCAGAGAGATGATATGTTCTTAATATACAGAAATTCACAC 519
QY 61 ACTAAGTATGATCTCTCATGAAAGAAATCTCAAAATATATGACAGAACTGTACAACTT 120
DB 520 ACTGAGCATGATGCTGACATGGAAGAAATCTCAAAATACATACGGAACCTACAACTGA 579
QY 121 TCTATCAGCTTGCCTTTTTCAGTCTGAGACACACAAATGAGGCTTTTGTGCGCTG 180
DB 580 TCAATCAGGCTGTCTCTTCCATCCCTCCGAGACAAATGTGAGCATGCTGTGCTCTG 639
QY 181 AAATGAGACACTGGAGA---TGCTGCTCTCCCTACCTTTCAATATAGATGCACAACT 237
DB 640 CAATGTGACCCAGAACGACACTGCTTTTCTCCCTACCTGTAATATATGATSCAAAGCA 699
QY 238 AAGGATTAAGAGCCAGAACGACACTTCCCTGATTTGCGCTGTACTGTATGTTT 297
DB 700 CCTGTGCAACCCCTGTCCAGACACACATCTGTGATTTGACGCTCTACTGTGAACAGTG 759
QY 298 GTTGTGTTTGTGGAGTGTCTCTTAAACACTAAGGAAAGGAAAGAGAGAGAGCT 357
DB 760 GTCTGTGTGTGGATGTTGCTTTTGAACACTAAGGAAAGGAAAGAGAGAGAGCT 819
QY 358 GGCCTCTCATGAT---GTGAACCATCAAAAGGAGAGAAAGAGAGAGAGAGAGAGC 414
DB 820 GGCCTCTCAATGAATGTGTGAACCATCAAAATGAAGAGAGAGAGAGAGAGAGAGC 879
QY 415 AAGCAAGAGTACATACAGCTACCTGAGATGATGATGAAGCCAGCTG---TATTAC 471
DB 880 AAGACAGAGCA-----GAAGTCATAGACATGTGATGATGCCAGTGTGATGTTAAT 933
QY 472 ATTTGAAGACAGCCTCAGGCGCAAAAGTACTACACA 509
DB 934 ATTTTAAAGACAGCCTCAGATGACAAAGTACTACAGA 971
RESULT 7
AF344851 1044 bp mRNA linear PRI 06-SEP-2001
LOCUS Macaca nemestrina CD86 protein precursor, mRNA, complete cds.
DEFINITION AF344851
ACCESSION AF344851
VERSION AF344851.1 GI:13655490
KEYWORDS p15-tailed macaque.
ORGANISM Macaca nemestrina
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 1044)
Villinger,F., Bostik,P., Mayne,A.E., King,C.L., Genain,C.P.,
Weiss,W.R. and Ansari,A.A.
AUTHORS Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas ligand and co-stimulatory molecules
JOURNAL Immunogenetics 53 (4), 315-328 (2001)
MEDLINE 21383618
PUBMED 11491535
REFERENCE 2 (bases 1 to 1044)
Villinger,F.
AUTHORS

TITLE Direct Submission
JOURNAL Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory
University School of Medicine, Winship Cancer Institute, 1365B
Clifton Rd, Atlanta, GA 30322, USA
FEATURES Location/Qualifiers
source 1..1044
/organism="Macaca nemestrina"
/db_xref="taxon:9545"
sig_peptide
CDS
/note="B7.2"
/codon_start=1
/product="CD86 protein precursor"
/protein_id="AAK37611.1"
/db_xref="GI:13655491"
/translation="MGISNLPFMAFLLSGAAPLKIQAVFNENADLPQOFANSONRSL
SELVVFQWQENLVLENYLIGKPKPSVYSKYRGTRRPESNTLRLRLQIKDKGLY
QCLIHKRPGLMIRIHOMSELSVLNFSOPELVLPSNTENNTLNLTSSIHGPEP
EKMSVLRKNTSEIDYGVWQKQDVTLELVYSLSVSPDVTSNMTIFCVLETDK
TQLSSPFSIELEDPPDPDHPMTAVLPSVVICVMARCLILMKKKKKKPPRNSYKC
GNTMRRESEOTKKREKINVPERSDEACVFKSLKTPSCDKSDTRF"
BASE COUNT 320 a 230 c 208 g 286 t
ORIGIN
Query Match 42.3% ; Score 215.2 ; DB 9 ; Length 1044 ;
Best Local Similarity 69.3% ; Pred. No. 1e-49 ;
Matches 356; Conservative 0; Mismatches 143; Indels 15; Gaps 4 ;
QY 1 ATACAAGTTACCCAGAACCTAAGAGATGATATTTTACGTAACCTGAAATTAACCT 60
DB 465 ATACAGGTTACCCAGAACCTGAGAAAGATGATGTTGTAAGAACCAAGAAATTCACCT 524
QY 61 ACTAAGTATGATCTCTCATGAAAGAAATCTCAAAATATGATGACAGAACTGTACAACTT 120
DB 525 ATCAGATGATGTTGTTATGCAAGAAATCTCAGATATATGTCACAGAACTGTGACAGTT 584
QY 121 TCTATCAGCTTGCCTTTTTCAGTCCCTGAAG---CACACATGTGAGCGTCTTTTGCC 177
DB 585 TCCATCAGCTTGTCTGTTTATTCCTCGATGTACGAGCAACATGACCAATCTCTGTGT 644
QY 178 CTGAACCTGAGACACTGAGAGATGCTGCTCCCTACCTTCTCAATATGATGACAACT 237
DB 645 CTGGAACCTGACA---AGACACAGCTTTTATCTCAGCTTTCTCTATAG-----AGCTT 695
QY 238 AAGGATTAAGACCTGGAACAAGGCACTTCTGTGATTCGGGCTGTACTGTATGTTT 297
DB 696 GAGGACCTCAGCGCTCCCGACAGACACATCCCTGTGATTCAGCTGTACTCATCAGTT 755
QY 298 GTTGTGTTTGTGGAGTGTCTCTTAAACACTAAGAAAGAGAGAGAGAGAGAGCCT 357
DB 756 GTTATATGTTGTGATGGCTTTCTGTCTAATTTCTATGAAAGTGAAGAAAGAGAGCAACT 815
QY 358 GGCCTCTCATGATGATGAAACATCAAAAGGAGAGAGAAAGAGAGCAAGAGCAACCT 417
DB 816 CGCAGCTCTTATAATGTGGAACACACATGAGAGGAGAGAGAGAGAGAGAGAGAG 875
QY 418 GAAAGTACATACACAGCTACCTGAGAGATCTGATGAAGCCAGCTG---TATTACATTT 474
DB 876 AAAAGAGAAAAAATTATATGATGATGAGAAAGATCTGATGAGAACCCCAATGTGTTTAAAGT 935
QY 475 TTGAAGACAGCCTCAGGCGCAAAAGTACTACAC 508
DB 936 TTGAAGACACCTTCATGCGCACAAAGAGATACAC 969
RESULT 8
AF344857 1048 bp mRNA linear PRI 06-SEP-2001
LOCUS Macaca mulatta CD86 protein precursor, mRNA, complete cds.
DEFINITION AF344857
ACCESSION AF344857
VERSION AF344857.1 GI:13650011
KEYWORDS
SOURCE thesus monkey.

QY 421 AGATACCATACCACTGAGATCTGATGAGAGCCAGTGTATTACATTTTGAG 480
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Db 1143 AGAGTACCATACCACTGAGATCTGATGAGAGCCAGTGTATTACATTTTGAG 1202
|||||
QY 481 ACAGCCTCAGGCGACAAAGTACTACACA 509
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Db 1203 ACAGCCTCAGGCGACAAAGTACTACACA 1231
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RESULT 3
AF157827 1138 bp mRNA linear MAM 08-MAY-2000
LOCUS AF157827
DEFINITION Feline CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
ORGANISM
cat.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
AUTHORS Chou, I.-S., Hash, S.M., Winslow, B.J. and Collisson, E.W.
TITLE Sequence analyses of feline B7 costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE 20180222
PUBMED 10713336
REFERENCE
AUTHORS Chou, I.-S., Hash, S., Winslow, B.J. and Collisson, E.W.
TITLE Direct Submission
JOURNAL Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 Km. 222, College Station, TX 77843, USA
FEATURES
source
1. .1138
Location/Qualifiers
/organism="Felis catus"
/db_xref="taxon:9685"
1. .1138
gene
/gene="CD86"
63. .1052
/gene="CD86"
/note="B7-2 antigen"
/product="CD86 antigen"
/codon_start=1
/protein_id="AA042974.1"
/db_xref="GI:5381424"
/translation="MGICDSITGMLSHLLVMAALLLSVSSMSQAYFNKGTGELPCHFT
NSONISLDELIVFWDQDKLVLEYLRGENQNVHRYKGRTSFDKDNMTLRHNIQI
IKDGYHCFIHYKGRGLVPMHOMSDLSVLANSFOPETTVTSNRTEGSLINLHVS
SIOGYEPKEMFVLTENSTKYDVMKSSONNTYELNVSISLFSVPEANVSIFC
CALKIETLEMLSLPRNIDAPKDKPDSCHFLMIAVLVFMVFYCGMVSFKLRKRK
KKOPGSHDEETIKREKESKOTNERVPHVPERSDACVNLKTSAGDKNO"
BASE COUNT 358 a 245 c 246 g 289 t
ORIGIN
Query Match 97.8%; Score 497.8; DB 4; Length 1138;
Best Local Similarity 99.6%; Pred. No. 4.7e-129;
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 241 GATAAAGACCCGTGACAAAGCCACTTCTCGATTGCGGCTGTACTGTATTTGTT 300
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Db 786 GATTAAGACCCGTGACAAAGCCACTTCTCGATTGCGGCTGTACTGTATTTGTT 845
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QY 301 GTTTTGTGGAGTGTCTCTTTAAACACTAAGCAAGAAAGAAAGCAAGCCTGGC 360
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Db 846 GTTTTGTGGAGTGTCTCTTTAAACACTAAGCAAGAAAGAAAGCAAGCCTGGC 905
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QY 361 CCCCTCATGAATGTGAACCATCAAAAGGAGAGAAAGCAACACCAACGAA 420
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Db 906 CCCCTCATGAATGTGAACCATCAAAAGGAGAGAAAGCAACACCAACGAA 965
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QY 421 AGATACCATACCACTGAGATCTGATGAGAGCCAGTGTATTACATTTTGAG 480
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Db 966 AGATACCATACCACTGAGATCTGATGAGAGCCAGTGTATTACATTTTGAG 1025
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QY 481 ACAGCCTCAGGCGACAAAGT 501
|||||
Db 1026 ACAGCCTCAGGCGACAAAGT 1046
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RESULT 4
AF106826 1897 bp mRNA linear MAM 14-DEC-1999
LOCUS AF106826
DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
ACCESSION AF106826
VERSION AF106826.1 GI:6572516
KEYWORDS
SOURCE
dog.
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Yang, S. and Sim, G.K.
TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20093996
REFERENCE
AUTHORS Yang, S. and Sim, G.-K.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
FEATURES
source
1. .1897
Location/Qualifiers
/organism="Canis familiaris"
/db_xref="taxon:9615"
/cell_type="peripheral blood mononuclear cells"
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/gene="CD86"
1. .5
5' UTR
/gene="CD86"
6. .995
CDS
/gene="CD86"
/function="counter-receptor for CD28 and CD152 (CTLA4)"
/product="B7-2 protein"
/codon_start=1
/protein_id="AA01297.1"
/db_xref="GI:6572517"
/translation="MYLRCTMELNLLFVMTLLLYGAASKSQAYFNKGTGELPCHFTN
SONISLDELIVFWDQDKLVLEYLRGENQNVHRYKGRTSFDKDNMTLRHNIQI
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SIOGYEPKEMFVLTENSTKYDVMKSSONNTYELNVSISLFSVPEANVSIFC
VLOESMLPSLPRNIDHTAETPDGDHILMIAVLVLMVFYCGMVSFKLRKRK
PGPSHDEETIKREKESKOTNERVPHVPERSDACVNLKTSAGDNSTTGP"
3' UTR
BASE COUNT 585 a 400 c 383 g 529 t
ORIGIN
Query Match 72.7%; Score 369.8; DB 4; Length 1897;
Best Local Similarity 85.7%; Pred. No. 4.1e-93;

FEATURES

source

Location/Qualifiers

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/db_xref="taxon:9685"

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/gene="CD86"

179..1177

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/note="CD28/CTLA4 counter receptor; B7-2 protein"

/codon_start=1

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/protein_id="AA023342.1"

/db_xref="GI:15418726"

/translation="MGICDSTMGLSHTLLVMALLSGVSSMKSOAYENKTELPCHFT
NSONTSLDELVEWODOKLYLEIFRKGKNPOVHLKYKRTSPDKNMTLRILNVO
IKDKGYHCFIHYKPKGLVPMHOMSSDLSVLANSQPEITVSNRENSGIIINTCS
SIQGYPERKEMFQLTENSTYKDYTKRSONNVLELVNVSISPEVPAHNVSVF
CALKLETEMLISLPENIDAPKDPQGHFLWLAVALVMEVFCGVSVFKLRKK
KKQPGSHCECTIKRERESKOTNERVPHVPERSDPAOCINILKTASGDKSTTHP"

BASE COUNT 877 a 570 c 586 g 797 t

ORIGIN

Query Match 100.0%; Score 509; DB 4; Length 2830;
Best Local Similarity 100.0%; Pred. No. 3 4e-132;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATACAAGTTACCCAGAACCTAAGAGATGTAATTTTCAGCTAAACACTGAGATTCAACT 60
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662 ATACAAGTTACCCAGAACCTAAGAGATGTAATTTTCAGCTAAACACTGAGATTCAACT 721
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61 ACTAAGTATGATCGTATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAAGCTT 120
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722 ACTAAGTATGATCGTATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAAGCTT 781
|||||
121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAACACACATGAGCGTCTTTTGCCCTG 180
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782 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAACACACATGAGCGTCTTTTGCCCTG 841
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181 AAACGTGGAACATGAGATGCTGCTCCCTACCTTCAATATGATGACAACTAAG 240
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842 AAACGTGGAACATGAGATGCTGCTCCCTACCTTCAATATGATGACAACTAAG 901
|||||
241 GATAAAGACCTGGAACAGGCGACCTCCCTGATGAGTGGGCTGATGTAATTTGTT 300
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902 GATAAAGACCTGGAACAGGCGACCTCCCTGATGAGTGGGCTGATGTAATTTGTT 961
|||||
301 GTTTTGTGGGATGTGTCCTTTTAAACACTAAGAAAGAAAGAAAGCAAGCCTGGC 360
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962 GTTTTGTGGGATGTGTCCTTTTAAACACTAAGAAAGAAAGAAAGCAAGCCTGGC 1021
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361 CCCCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAAGAA 420
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1022 CCCCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAAGAA 1081
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421 AGAGTACCATCCAGTACCTGAGAGATCGATGAGCCCAAGTATATTAACATTTTGAAG 480
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1082 AGAGTACCATCCAGTACCTGAGAGATCGATGAGCCCAAGTATATTAACATTTTGAAG 1141
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481 ACAGCTTCAGGCGCAAAAGTACTACACA 509
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1142 ACAGCTTCAGGCGCAAAAGTACTACACA 1170
|||||

RESULT 2

AB030652 1270 bp mRNA linear MAM 01-MAR-2001

DEFINITION Felis catus mRNA for B-lymphocyte activation antigen B7-2 (CD86), complete cds.

ACCESSION AB030652

VERSION AB030652.1 GI:9796387

KEYWORDS B-lymphocyte activation antigen B7-2 (CD86).

SOURCE *Felis catus peripheral blood mononuclear cell cDNA to mRNA.

ORGANISM Felis catus

REFERENCE

AUTHORS

1 (sites)

Nishimura,Y., Shimojima,M., Miyazawa,T., Sato,E., Nakamura,K., Izumiyu,Y., Ikeda,Y., Mikami,T. and Takahashi,E.

1994

Molecular cloning of the cDNAs encoding the feline B-lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA-4-Ig

Eur. J. Immunogenet. 27 (5-6), 427-430 (2000)

JOURNAL

2465322

2 (bases 1 to 1270)

REFERENCE

AUTHORS

Nishimura,Y.

Submitted

Direct Submission

Submitted (31-Jul-1999)

The University of Tokyo, Department of Veterinary Microbiology, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan

(E-mail: yorihito@erccoc.ou.ac.jp, Tel: +81-3-5841-5396, Fax: +81-3-5841-8184)

Sequence updated (08-Jun-2000).

FEATURES

Location/Qualifiers

1..1270

/organism="Felis catus"

/db_xref="taxon:9685"

/cell_type="peripheral blood mononuclear cell"

240..1238

/gene="CD86"

240..1238

/codon_start=1

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/protein_id="BAB11688.1"

/db_xref="GI:9796388"

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CALKLETEMLISLPENIDAPKDPQGHFLWLAVALVMEVFCGVSVFKLRKK
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polyA_signal 1245..1250

BASE COUNT 378 a 281 c 260 g 351 t

ORIGIN

Query Match 99.7%; Score 507.4; DB 4; Length 1270;
Best Local Similarity 99.8%; Pred. No. 9.6e-132;
Matches 508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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61 ACTAAGTATGATCGTATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAAGCTT 120
|||||
783 ACTAAGTATGATCGTATGAAGAAATCTCAAAATAATGTGACAGAACTGTACAAGCTT 842
|||||
121 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAACACACATGTAAGCGTCTTTTGCCCTG 180
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843 TCTATCAGCTTGCCCTTTTTCAGTCCCTGAAACACACATGTAAGCGTCTTTTGCCCTG 902
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361 CCCCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAAGAA 420
|||||
1083 CCCCTCATGATGTGAACCATCAAAAGGAGAGAAAGGACCAACAGACCAAGAA 1142
|||||

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 696.962 Seconds
(without alignments)
15282.914 Million cell updates/sec

Title: ' US-09-646-561-30

Perfect score: 509
Sequence: 1 atacaaggtaccacgaacc.....ggcgacaaagttactacaca 509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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2: gb_htg:*
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32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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3	497.8	97.8	1138	4	AF157827		AF157827	Felis cat
4	369.8	72.7	1897	4	AF106826		AF106826	Canis fam
5	268.8	52.8	994	4	PIGCD865		PIGCD865	Sus scrofa
6	268.8	52.8	994	6	AX027016		AX027016	Sequence
7	215.2	42.3	1044	9	AF344851		AF344851	Macaca ne
8	215.2	42.3	1048	9	AF344857		AF344857	Macaca mu
9	212.6	41.8	972	6	AX027005		AX027005	Sequence
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15	212.6	41.8	1120	6	AR112747		AR112747	Sequence
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17	212.6	41.8	1120	6	AX047043		AX047043	Sequence
18	212.6	41.8	1161	6	AR146414		AR146414	Sequence
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23	210.4	41.3	1062	9	AF344861		AF344861	Sequence
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33	110	21.6	751	6	AR147737		AR147737	Sequence
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36	109.8	21.6	737	6	HSB72S5		HSB72S5	Human CTFLA-
37	99	19.4	210	6	AR146418		AR146418	Sequence
38	85	16.7	133	4	AF222915		AF222915	Sus scrofa
39	77.2	15.2	418	10	MMB72G08		MMB72G08	Mus musculu
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ALIGNMENTS

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LOCUS	AY007704				
DEFINITION	Felis catus CD86 (CD86) mRNA, complete cds.				
ACCESSION	AY007704				
VERSION	AY007704.1				GI:15418725
KEYWORDS					
SOURCE					
ORGANISM	Felis catus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	1 (bases 1 to 2830)				
AUTHORS	Yang,S., Sellins,K.S., Powell,T., Stoneman,E. and Sim,G.K.				
TITLE	Novel transcripts encoding secreted forms of feline CD80 and CD86				
JOURNAL	costimulatory molecules				
MEDLINE	Vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)				
PubMed	21390213				
REFERENCE	2 (bases 1 to 2830)				
AUTHORS	Yang,S.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-SEP-2000) Immunology, Heska Corporation, 1613				
	Prospect Parkway, Ft Collins, CO 80525, USA				

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Db 1109 CATGCGACAAAGTATACATGTTT 1134

Search completed: October 19, 2002, 23:35:57
Job time : 44.5402 secs


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: NAME: Mandragouras, Amy E.
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: RPI-002CP2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 742-4214
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1120 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 107..1093
: US-08-403-253A-3

Query Match          54.2%; Score 540; DB 4; Length 1120;
Best Local Similarity 75.4%; Pred. No. 1.4e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

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DB 120 GCACATATGGAGCTGAGTACACTCTCTCTGATGGCCCTCCTGCTCTGTTCTT 179
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DB 180 CTCTGAAGATTCAGCTTATTTCAATGAGACTGCAGACCTGCCATGCCATTGGCAACT 239
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DB 240 CTCAAACATTAAGCCGTGAGCTGAGTATTTTGGCAGACACAGATTAAGCTGCTC 299
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RESULT 13
PCT-US95-02576-22
: Sequence 22, Application PC/TUS9502576
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street, suite 510
: City: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/02576
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/205,697
: FILING DATE: 02-Mar-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Mandragouras, Amy E.
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: BWI-120CPPC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1120 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 107..1093
: PCT-US95-02576-22

Query Match          54.2%; Score 540; DB 5; Length 1120;
Best Local Similarity 75.4%; Pred. No. 1.4e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCACATATGGAGCTGAGTACACTCTCTGATGGCCCTCCTGCTCTGTTCTT 76
DB 120 GCACATATGGAGCTGAGTACACTCTCTGATGGCCCTCCTGCTCTGTTCTT 179
QY 77 CCATGAAGATCAAGCATATTTCAACAGAGCTGGAGAACTGCCATTGTTTACAACT 136

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Db	777	--AGAGCGGGCTTTATATCTTCAACCTTTCCTATAG-----AGCTTGAGGACCCAC	827
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Db	828	CTCCCCAGACACATTCCTTGATTCACCTGTACTCTCCAAAGTATTTATTTGTGTGA	887
QY	794	GGATGTTGTCCTTTTAAACACTAAGAAAAAGAAAGAAGCAGCCGTGGCCCTCATG	853
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QY	854	AATGTGAACCATTAATAAAGSAGAGAAAAGAGACCAACAGAAAGATGTCCT	913
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Db	1068	CATCGACAAAAGTATGATCATGTTT	1093

RESULT 9

US-08-280-757B-1
; Sequence 1, Application US/08280757B

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.
; ;
APPLICANT: Nadler, Lee M.
; ;

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; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Ed

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;
; TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510

CITY: Boston
STATE: Massachusetts

COUNTRY: USA
ZIP: 02109

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; PATENT INQUIRY NUMBER: 100 100 100
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APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PUBLICATION NUMBER: 00401 004

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APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/100,303

APPLCATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773

ATTORNEY/AGENT INFORMATION:
FILING DATE: 3-NOV-1993
AFFILIATION NUMBER: 08/14/113

PERSONNEL/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36 207

7 REFERENCE/DOCKET NUMBER: RPI-004CP2
8
9 TELECOMMUNICATION INFORMATION:
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840

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1120 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 107..1093
US-08-280-757B-1

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Query Match	54.28;	Score 540;	DB 3;	length 1120;
Best Local Similarity	75.48;	Pred. No. 1.4e-160;		
Matches 743; Conservative	0;	Mismatches 225;	Indels 18;	Gaps 5;

QY	17	GCATATATGGGACCTGAGGTCACACACCTCCCTGTGTGATGGCCCTCCCTGCTCTCTGAGTGTTC	76
Dd	120	GCATATATGGGACCTAGATTAACATCTCTCTTGTGTATGGCTCTCTGCTCTCTGAGGCTGCTC	179
QY	77	CCATGAGAGGTCGAAGCATATTTTCAACAAGCTGGSAGACTGCGATCCCATTTTACAAC	136
Dd	180	CTCTGAAGATTCAAGCTTATTTTCAATGAGACTCCAGACCTGCGATCCCAATTTGGCAACT	239
QY	137	CTCAAAACATTAAGCCTTGATGAGCTGGTGTATATTTTGGCAGGCCGAGATTAAGCTGTTC	196
Dd	240	CTCAAAACCAAAGCCTTAGTAGACTAGTACTATTTTGGCAGGCCGAGAAACTTGGTTC	299
QY	197	TGTATGAGATATTTCAGAGCCAAAGAGAACCCCTCAAAATGTTTCATCTCAATATTAAGGCC	256
Dd	300	TGATGAGGATTACTATTGAGCAAGAGAAATTTACAGTGTTCATTCAGATATTATGAGGCC	359
QY	257	GTACAGCTTTGACACGAGCACTGGACCTGTAGACTCCACAATGTTCAGATCAAGGACA	316
Dd	360	GCACAACTTTTGATTCGAGCAGTTGGACCTGTAGACTTCACATCTTCAGATCAAGGACA	419
QY	317	AGGGCACAATTCACCTGTTTCATTCATTAATTAAGGGCCAAAGAGACTAGTCCCATGCAAC	376
Dd	420	AGGGCTTGTATCAATGTATATATCATCAACAAAGGCCACAGGAATGATTCGATCCAC	479
QY	377	AAATGACTTTCGACCTATACAGTCTGCTGCTAACTTCAGTCAACCTGAAATTAAGACTACT	436
Dd	480	AGATGATTTCTGAACCTGCTGCTGTGCTACTTCAGTCAACCTGAAATTAAGACAATT	539
QY	437	CTAATACACAGAAATTTCTGCATCATTAATTTGACCTGCTCATCTATACAGGTTACC	496
Dd	540	CTAATATTAACAGAAA--TGTGTACATTAATTTTGACCTGCTCATCTATACAGGTTACC	596
QY	497	CAGAACCTAAGGAGATGTTATTTTCAGTGAACCTGAGAAATTCACCTACTAGTATGATA	556
Dd	597	CAGAACCTAAGGAGATGAGTGTGTTGCTAAGAACCAAGAAATTCACCTACTAGTATGATG	656
QY	557	CTGCACTGAGAAATCTCAAAATTAATGTGACAGAACTGTACAACTTCTACACTGTGC	616
Dd	657	GTATTAAGCAAAATCTCAGATTAATGTGACAGAACTGTACAACTTCTACACTGTGT	716
QY	617	CTTTTCAGTCCCTGAAG--CACACAATGTGACGCTCTTTGTGCCCTGAATCTGAGGA	673
Dd	717	CTTTTCATTCCTCGATGTACAGCAAAATGATGCATCTTGTATTTGGAACTGACA	776
QY	674	CACGTGAGATGCTGCTCTCCCTACCTTTCAATTTAGATGACACAACCTAAGGATTAAGAC	733
Dd	777	--AGACGGGCTTTATCTTCACTCACTTTCTCTAATG----AGCTGAGGACCTCTACGC	827
QY	734	CTGAACAGGCACTCTCTCTGTGATGCGGCTGTACTTGAATGTTGTGTTTGTG	793
Dd	828	CTCCCCAGACACATCTCTGTGATTAACAGCTGTACTTCCAACAGATTAATATGTGTGA	887
QY	794	GGATGCTCTTTAAAAACCTAAGSAAAAAGACAGACAGCAAGCCTGCGCTCTCATG	853
Dd	888	TGGTTTTCTGTAAATTTCTATGAAATTTGAGAAAGAAAGAGGCGCTGCACTCTTATA	947
QY	854	AATGTGAACCATCAAAAGSAGAGAAAGAGAGCAACAAGACCAAGAAAGATGATCAT	913
Dd	948	AATGTGAACCAACAATGAGAGAGGAGAGAGATGAACAGCAAGAAAGAGAAAAA	1007
QY	914	ACCACTGATGAGATCTGATGAGACCCAGT--TATTAACTTTTGAAGACAGACT	970
Dd	1008	TTCATTAAGTATGATGAGAAAGCCAGCGTCTTTTAAAAAGTTTGAAGACATCTT	1067
QY	971	CAGGCGACAAAAGTACTACATTTT	996

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OY 437 CTAATGAAAGCAAAATTTGTGGCACAATTAATTTGAGCTGCTCATCTATATCAAGGTTACC 493
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 540 CTAATATATACAGAAAA---TGTGTACATTAATTTTGAGCTGCTCATCTATACAGGTTACC 596
OY 497 CAGAACCTAAGAGAGATGATTTTTCAGCTAAACACTGAGAAATTCACACTACTAAGTATGATA 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 597 CAGAACCTAAGAGAGATGATGTTTGGCTAAGAACCAAGAAATTCACACTATGAGATGATG 656
OY 557 CTGTCATGAAGAATTCACAAATTAATTAATGTGACAGAACGTACACGTTTCAATGAGCTGC 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 GTATTATTCAGAAATCTCAAGATATATGTCACAGAACTGTACGAGTTTCCATCAGCTTGT 716
OY 617 CTTTTTCAGTCCCTGAAG---CACACAATGTGAGCCCTCTTTTGTGCCCTGAACCTGAGAGA 673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 CTGTTTCATTCCTCGATGTATGTCAGACAATATGACCATCTCTGTATCTGTGAAACGTGACA 776
OY 674 CACTGAGATATGCTGCTCTCCCTACCTTTCAATATATATGCACAACTAAGGATTAAGACC 733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 777 ---AATCCCGGCTTTTATCTTCACCTTTCCTATAG-----ACCTTGAGAGCCCTCAGC 827
OY 734 CTGAACAAGGCGCACCTCTCTCGAATGTGGGCGTGTACTTGTAAATGTTGTTGTTTTTGTG 793
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 828 CTCCCCCAGACACACTTCTTGGAATTTACAGCTGTACTTCCAAACGTTATTTATGTGTGA 887
OY 794 GGATGCTGTCTTTAAACACTAAGAAAAAGAGAAAGACAGACCTTGCCCTCTCATG 853
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 888 TGGTTTCTGTCTAATTTCTATGAAATGGAAGAGAGAGAGAGCGGCTCGCAACTCTATA 947
OY 854 AATGTGAACCATCAAAAGGAGAGAAAAAGAGACAAACAGCAACGAAGAGCTACAT 913
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 948 AATGTGGAACCAACACATGAGAGGAGAGAGTGAACAGACCAAGAAAGAGAAAAA 1000
OY 914 ACCAGCTACTGAGAGATCTATGAAGCCAGTG---TATTAACTATTTGAACACAGCCT 970
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1008 TCCATATACCTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTGCAAGCATCTT 1066
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 971 CAGCGGACAAAAGTACTACATTTT 996
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1068 CATGCGACAAAAGTATACATGTTT 1093
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RESULT 8
US-08-479-744A-1
: Sequence 1, Application US/08479744A
: Patent No. 6084067
: GENERAL INFORMATION:
:   APPLICANT: Freeman, Gordon J.
:   APPLICANT: Nadler, Lee M.
:   APPLICANT: Gray, Gary S.
:   TITLE OF INVENTION: No. 6084067e1 CTL44/CD28 ligands and
:   TITLE OF INVENTION: Uses Therefor
:   NUMBER OF SEQUENCES: 55
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: LAHIVE & COCKFIELD, LLP
:     STREET: 60 State Street
:     CITY: Boston
:     STATE: Massachusetts
:     COUNTRY: USA
:     ZIP: 02109
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patentln Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/479,744A
:     FILING DATE: June 7, 1995
:     CLASSIFICATION: 435
:     PRIOR APPLICATION NUMBER: 08/280,757
:     FILING DATE: 26-JUL-1994
:     APPLICATION NUMBER: 08/109,393
:     FILING DATE: 28-AUG-1993

```

	APPLICATION NUMBER:	08/101,624	
:	FILING DATE:	26-JULY-1993	
:	APPLICATION NUMBER:	08/147,773	
:	FILING DATE:	3-NOV-1993	
:	ATTORNEY/AGENT INFORMATION:		
:	NAME:	Mandragouras, Amy E.	
:	REGISTRATION NUMBER:	36,207	
:	REFERENCE/DOCKET NUMBER:	RPI-004CP3	
:	TELECOMMUNICATION INFORMATION:		
:	TELEPHONE:	(617) 227-7400	
:	TELEFAX:	(617) 227-5941	
:	INFORMATION FOR SEQ ID NO:	1:	
:	SEQUENCE CHARACTERISTICS:		
:	LENGTH:	1120 base pairs	
:	TYPE:	nucleic acid	
:	STRANDEDNESS:	single	
:	TOPOLOGY:	linear	
:	MOLECULE TYPE:	cDNA	
:	FEATURE:		
:	NAME/KEY:	CDS	
:	LOCATION:	107..1093	
:	US-08-479-744A-1		
Query Match	54.2%;	Score 540;	DB 3; Length 1120;
Best Local Similarity	75.4%;	Pred. No. 1,4e-160;	
Matches 743; Conservative	0;	Mismatches 225;	Indels 18; Gaps
Oy	17 GCACATAGGGACCTGTCACACTCCTCTTGATGGCCCTCGCTCMGTGTTTCTT	76	
Dd	120 GCACATATGGACCTGAGTAACATTCTTTTGATGGCTTCCTCTCTGCTGCTC	179	
Oy	77 CCATAGAGAGTCACGATATTTTCAACAAGACTGGAGAATGCCATTTTACAAC	136	
Dd	180 CTCGTAAAGATTCAGACTATTTCATGAGACTGCAGACTCCATGGCAAATTTCCA	180	
Oy	137 CTCAAAACATAAGCCTGSATAGCTGGTAGATTTTGGCAGGACAGAGTAAGCTG	196	
Dd	240 CTTCAAAACCAAGCTGTAGTGAAGTATTTTGGCAGGACAGAGTAAGCTG	239	
Oy	197 TGTATGATATATTCAGAGCCAAAGAAACCCTCAAAATGTTTCATCTCAAA	256	
Dd	300 TGAATGAGGTATTTAGTACCAAGAGAAATTTGACAGTGTTCATTCCAGATAT	359	
Oy	257 GTACACACTTTGACACAGGACAACTGAGCCCTGACATCCAAATGTCAGATCA	316	
Dd	360 GCACAGTTTTGATTCGACAGCTGGACCTGAGACTTCACAACTTCAGATCA	419	
Oy	317 AGGCGACATATCACGTGTTTCATTATTAAGAGGCCCAAGAGCTATGCCATG	376	
Dd	420 AGGCGTGTATCATATGATATCATTCATCAAAAAGCCOACAGGAATGTTCC	479	
Oy	377 AATGATGTTTGACCTATCACTGCTGTTGCTAACCTTCAGTCAACCTGAATTA	436	
Dd	480 AGATTAATTTTGAACCTGCACTGCTGTTGCTAACCTTCAGTCAACCTGA	539	
Oy	437 CTAATAGAACAGAAATCTGGCATCAATAAATTTGACCTGCTCATCTATCA	496	
Dd	540 CTAATATATACAGAAAA--TGTGATACATAAATTTGACCTGCTCATCTA	596	
Oy	497 CAGAACCTAAGAGAGTATTTTCAAGCTAAACACTGAGAAATTCACACTA	556	
Dd	597 CAGAACCTAAGAGAGTATTTTCAAGCTAAACACTGAGAAATTCACACTA	656	
Oy	557 CTGTCATGACAGAAATCTCAAAATATGTGACAGAACTGTACACGTTTCTA	616	
Dd	657 GTATATATCAAGAAATCTCAAAATATGTGACAGAACTGTACACGTTTCT	716	
Oy	617 CTTTTCAGTCCCGAGG--CAACAATGTGAGCCGCTTTTGGCCCTGAAC	673	
Dd	717 CTTTTCAGTCCCGAGG--CAACAATGTGAGCCGCTTTTGGCCCTGAAC	776	
Oy	674 CACTGGAAATCTGCTCTCCCTACCTTTCAATATAGATGACAAACCTA	733	

REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
AMT-SENSE: NO
US-09-039-762A-33

Query Match 54.2%; Score 540; DB 4; Length 1002;
Best Local Similarity 75.4%; Pred. No. 1.3e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

OY 17 GCACATAGGAGCTGAGTCACTCTCTCTGTGATGGCCCTCCTGCTGCTGTTCTT 76
|||||
DB 20 GCACATAGGAGCTGAGTCACTCTCTGTGATGGCCCTCCTGCTGCTGTTCTT 79
OY 77 CCATGAGAGTCAACATTTTCAACAGACTGGAGACTGCCATTGTTTACAACT 136
|||||
DB 80 CTTCTGAAGATTCAAGCTTTTTCATGAGACGACGACCTGCCATTGCAATTTGCAACT 139
OY 137 CTCAAACATTAAGCTGGATGAGCTGCTGATTTTGGCAGACACAGATAGCTGTTTC 196
|||||
DB 140 CTCAAACATTAAGCTGGATGAGCTGCTGATTTTGGCAGACACAGATAGCTGTTTC 199
OY 197 TGTATGAGATATTTCAGAGGCAAGAACCTCAAAATGTTTCATCAATATAAGAGGC 256
|||||
DB 200 TGAATGAGTATCTAGTCAAGCAAGAAATTTGACAGTGTTCATTCGAAGTATAGGGCC 259
OY 257 GTACAAAGCTTTGACAGGCACTGACCTGACATGTCACATGTCGATCAAGGACA 316
|||||
DB 260 GCACAAAGTTTATTCGACAGTGGACCTGACCTGACCTCAAAATTCGACATCAAGGACA 319
OY 317 AGGCAATATCACTGTTTCATTTATTAAGGAGGCCCAAGAGTACTGTCATGACAC 376
|||||
DB 320 AGGCGTGTATCAATGTATATCATCATCAAAAGCCCAAGAGTATGTCATCCACAC 379
OY 377 AATGAGTTTGCAGCTATGAGTGTGCTTACTTACATGATCACTGAATATACAGTACTT 436
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DB 380 AGATGATTTCTGAAGTGTGCTTGTGCTTGAATCACTGAATATAGTACCAATTT 439
OY 437 CTAAATGAAGCAAAATTCGTGACATCAATTTGACCTGCTCATCTATACAAAGTTACC 496
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DB 440 CTAAATGAAGCAAAATTCGTGACATCAATTTGACCTGCTCATCTATACAGGTTACC 496
OY 497 CAGAACCTAAGAGATGATTTTTCAGCTAAACATGAGATTTCAACTACTAAGTATGATA 556
|||||
DB 497 CAGAACCTAAGAGATGATGTTTGGCTAAGAACCAAGAAATTCACATATCGAGTATGATG 556
OY 557 CTGTCTGAGAAATCTCAAAATATGTCAGCAAGACTGTACACGTTTCTATACCTTGC 616
|||||
DB 557 GTATTATGCAAAATCTCAAGATATGTCACAGAACTGTACAGCTTTCATCACTGCT 616
OY 617 CTTTTCAGTCCCTGAG--CACACAATGTAGGCTGTTTGGCCGGAAGTGGAGGA 673
|||||
DB 617 CTGTTTCATTCCTCTGATGTTTACGAGCAATATACCACTCTCTGATTTCTGGAACTGACA 676
OY 674 CACTGAGATGCTGCTCTCCCTACCTTTCATATAGATGACACAACTAAGTAAGAGAC 733
|||||
DB 677 ---AGACGGGGCTTTTATCTTCACCTTCTCTATAG-----AGCTGAGAGACCTCAGC 727
OY 734 CTGACAAAGCCACTCTCTGAGATGGCGCTGTAAGTGTAAATGTTTGTGTTTGTG 793
|||||
DB 728 CTCCCCCAACACCATCTCTGATGATGCTGATCTTCAAGCTTATATATATGATG 787
OY 794 GGATGCTGCTTTTAAACATAAGAAAGAAAGAGAGAGCTGGCCCTCTCATG 853
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DB 788 TGTGTTCTGCTAATTCTATGAAATGGAAGAAAGAGCGCTCGCACTCTTATA 847
OY 854 AATGTGAACCATCAAAAGGAGAGAAAGAGACAAACAGACCAAGCAAGAGTACCAT 913
|||||
DB 848 AATGTGAGACCAACACATGATGAGAGAGAGACTGAACAGACCAAGAAAGAGAAAAA 907
OY 914 ACCAGTACTGAGATCTGATGATGAGCCAGTG---TATTACATTTTGAACAGACCT 970
|||||
DB 908 TCCATATACCTGAAAGATCTGATGAAAGCCAGCTGTTTAAAGTTCAGACATCTT 967
OY 971 CAGCGACAAAGTACTACACATTT 996
DB 968 CATCGACAAAGTACTACATGTTT 993

RESULT 6
US-08-456-104-1
Sequence 1, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
CORRESPONDING ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-456-104-1

Query Match 54.2%; Score 540; DB 2; Length 1120;
Best Local Similarity 75.4%; Pred. No. 1.4e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

OY 17 GCACATAGGAGCTGAGTCACTCTCTGTGATGGCCCTCCTGCTGCTGTTCTT 76
|||||
DB 120 GCACATAGGAGCTGAGTCACTCTCTGTGATGGCCCTCCTGCTGCTGTTCTT 179
|||||

```

? APPLICANT: Sprent, Jonathan
? APPLICANT: Brumark, Anders
? APPLICANT: Jackson, Michael
? APPLICANT: Peterson, Per A
? TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
? TITLE OF INVENTION: ACTIVATION OF T-CELLS
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Olsson & Hierl, Ltd.
? STREET: 20 No. 6251627th Wacker Drive, Suite 3000
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentln Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/039,641
? FILING DATE: 8-MAR-1995
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Olsson, Arne M.
? REGISTRATION NUMBER: 30,203
? REFERENCE/DOCKET NUMBER: T5R14710
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 580-1180
? TELEFAX: (312) 580-1189
? INFORMATION FOR SEO ID NO: 33:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1002 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? US-09-039-641-33

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Query Match          54.2%; Score 540; DB 4; Length 1002;
Best Local Similarity 75.4%; Pred. No. 1.3e-160;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 17 GCACATATGGAGTGTACACTCTCTCTGATGGCCCTCCTGCTCTGCTGTTCTT 76
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 20 GCACATATGGAGTGTACACTCTCTGATGGCCCTCCTGCTCTGCTGTTCTT 79
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 77 CCATGAAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGCAATTTTCAACT 136
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 80 CTTCTAGAGTTTAACTTATTTCAATGAGACTGACAGCTGCCATGCCAATTTGCAACT 139
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 137 CTCAAACATAAGCCTGATGAGTGTAGTATTTTGGCAGAGCAGAGATAGCTGTTT 196
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 140 CTCAAACATAAGCCTGATGAGTGTAGTATTTTGGCAGAGCAGAGATAGCTGTTT 199
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 197 TGTATGAGATATTCAGAGGCAAGAAACCTCAAAATGTTTCATCTCAATATAAGGGCC 256
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 200 TGAATGAGGTATATCTAGGCAAGAAATTTGACAGTTCATCTCAAGTATATAGGGCC 259
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 257 GTACAAGCTTTGACAAGCAACTGAGCCCTGAGACTGCACATGTTCAAGTCAAGGCA 316
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 260 GACACAGTTTTCATTCGAGCACTTGACCTGAGACTTCACAAATCTTACATCAAGGCA 319
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 317 AGGCAACATATCACTGTTTCATCTTATTAAGGGCCCAAGGACTAGTTCCTCATGAC 376
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 320 AGGGCTTGATCAATGATCATCAATCAAAAGCCACAGAAATGATTTGGCATCCACC 379
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 377 AATAGATTCAGCTATCAAGGCTTGTCTAATCTAGTCAACCTGAATTAACAGTACTT 436
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 380 AGATGAATTCGAACTGACGTGCTTGTCTAATCTAGTCAACCTGAATTAACAGTACTT 439
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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QY 437 CTAATAGAACAGAAAATTTGTCATCAATAATTTGACCTGCTCATATCAAGGTTACC 496
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 440 CTAATATATACAGAAA---TGTGATCACTAAATTTGACCTGCTCATATCAAGGTTACC 496
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 497 CAGAACCTAAGAGATGATTTTTCAGCTAAACACTGAAATTCAGTACTAAGTAGATA 556
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 497 CAGAACCTAAGAGATGATGTTTGTCTAAGAACCAAGAAATTCAGTACTAAGTAGATG 556
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 557 CTGATGAGAACAAATTCGAAATTAATGAGACAGAGCTGCAACGTTTCATACAGTTCG 616
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 557 GTATTATGACAGAAATTCGAAATTAATGAGACAGAGCTGCAACGTTTCATACAGTTCG 616
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 617 CTTTTCAGTCCCTGAAG---CACACATGTGAGCCGCTTTTGTGCCCCGTAAGTGGAGA 673
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 617 CTTTTCATTCCTGATGTTTACGAGCAATATGACCATCTTCTGATTCGTGAAGACGACA 676
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 674 CACTGGAGATCTGCTCTCCCTACCTTCAATATAGTGCACAACTCAAGATTAAGACC 733
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 677 --AGAGCGGCGCTTTTATCTTCAACCTTTCCTATAG-----AGCTTGAGAGCCCTCAGC 727
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 734 CTGAACAGGCCCACTCTCCTGATTCGCGCTGACTTGTATATGTTTGTGTTTGTG 793
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 728 CTCCCCAGACACATTCCTTGGATTTACAGCTGACTTCCACAGTTATATATGTGTA 787
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 794 GGATGTGTCCTTTTAAACACTAAGAAAGAAAGAAAGAGAGCCCTGCCCCCTCAG 853
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 788 TGTGTTTCTGCTTAATTCATATGAAATGAAAGAAAGAGAGAGCCCTGCCCCCTCAG 847
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 854 AATGTGAACCATCAAAAGGAGGAAAGAAAGAGCAACAGACCAAGAAAGTACCAT 913
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DB 848 AATGTGAACCATCAACATGAGAGGAGGAGAGATGAAACAGACCAAGAAAGGAAAAA 907
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QY 914 ACCAGTACCTGAGAGATCTGATGAAGCCCAAGTG---TATTACATTTTGAAGACAGCT 970
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DB 908 TCCATATACCTGAAGATGATGATGAAGCCAGCGGTGTTTAAAGTGAAGACATCTT 967
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QY 971 CAGCGCAACAAAGTACTACATTTT 996
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 968 CATGCAACAAAGTATGATCATGTTT 993
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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RESULT 5
US-09-039-762A-33
; Sequence 33, Application US/09039762A
; Patent No. 6255073
; GENERAL INFORMATION:
; APPLICANT: Cal, Zelig
; APPLICANT: Sprent, Jonathan
; APPLICANT: Brumark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olsson & Hierl, Ltd.
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,762A
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OLSON, Arne M.
; REGISTRATION NUMBER: 30,203

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QY 364 GTTCCATGACCAAAATGAGTCTGACCTATACAGTCTGCTAACTGATGACCACTGAA 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 ATTCGATCCACCGATATTCGTAAGTGTGATGCTGCTGTAAGTGTGATGCTGTAAGT 549
QY 424 ATACAGTACTCTATATGAGACAGAAATCTGAGCATATATATGACCTGCTCATCT 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 550 ATAGTACCAATTTCTATATTAACAGAAA--TGATGATATTAATTTGACCTGCTCATCT 606
QY 484 ATACAGTACTCTATATGAGACAGAAATCTGAGCATATATATGACCTGCTCATCT 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 607 ATACAGTACTCTATATGAGACAGAAATCTGAGCATATATATGACCTGCTCATCT 666
QY 544 ACTAATGATGATCTGATGAGAAATCTGAAATATGATGACAGAACTGATACAGCTT 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 667 ATGATGATGATGATGATGAGAAATCTGAAATATGATGACAGAACTGATACAGCTT 726
QY 604 TCTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 727 TCTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 661 CTGAAACTGAGACACTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 787 CTGAAACTGAGACACTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837
QY 721 AAGGATAAAGACCTGATGAGAAATCTGAAATATGATGACAGAACTGATACAGCTT 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 838 GAGGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCT 897
QY 781 GTGATTTTGTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 898 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
QY 841 GGGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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Db 958 CGGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
QY 901 GAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
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Db 1018 AAGAGGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
QY 958 TTGAGACAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCT 996
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Db 1078 TCGAAGACATCTTCATGCGACAAAGATGATGATGATGATGATGATGATGATGAT 1116

RESULT 2
PCT-US94-09642-1
; Sequence 1, Application PC/TUS9409642
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
; TITLE OF INVENTION: Protein and Related Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation, M-3-W
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940-1000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh IIcx
; OPERATING SYSTEM: System Software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/120,606
; FILING DATE: 13-SEP-1993
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US 08/116,882
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0390K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7039
TELEFAX: 201-822-7398
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 152..1123
PCT-US94-09642-1

Query Match 55.5%; Score 553; DB 5; Length 1428;
Best Local Similarity 75.7%; Pred. No. 1,3e-164;
Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 4 GGCATTTGTGACAGCACTATGAGGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
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Db 134 GGCATTTGTGACAGCACTATGAGGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 193
QY 64 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
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Db 194 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
QY 124 CATTTTACAACTCTCAAAATGAGGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 254 CATTTTACAACTCTCAAAATGAGGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
QY 184 GATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
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Db 314 GAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
QY 244 AAATATGAGGCGGTGACAGCTTGCAGAGCACTGAGACCTGAGACCTGAGACCTGAGACCT 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 AAGTATGAGGCGGTGACAGCTTGCAGAGCACTGAGACCTGAGACCTGAGACCTGAGACCT 433
QY 304 CAGATCAAGGACAGGCGGTGACAGCTTGCAGAGCACTGAGACCTGAGACCTGAGACCTGAG 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 434 CAGATCAAGGACAGGCGGTGACAGCTTGCAGAGCACTGAGACCTGAGACCTGAGACCTGAG 493
QY 364 GTTCCATGACCAAAATGAGTCTGACCTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
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Db 494 ATTGCACTCCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
QY 424 ATACAGTACTCTATATGAGACAGAAATCTGAGCATATATATGACCTGCTCATCT 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 ATAGTACCAATTTCTATATTAACAGAAA--TGATGATATTAATTTGACCTGCTCATCT 610
QY 484 ATACAGTACTCTATATGAGACAGAAATCTGAGCATATATATGACCTGCTCATCT 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 611 ATACAGTACTCTATATGAGACAGAAATCTGAGCATATATATGACCTGCTCATCT 670
QY 544 ACTAATGATGATCTGATGAGAAATCTGAAATATGATGACAGAACTGATACAGCTT 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 671 ATGAGTATGATGATGATGATGAGAAATCTGAAATATGATGACAGAACTGATACAGCTT 730
QY 604 TCTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 731 TCTATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 790
QY 661 CTGAAACTGAGACACTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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Db 791 CTGAAACTGAGACACTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
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OM nucleic - nucleic search, using sw model

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(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-28

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Sequence: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCtus.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55.5	1424	4	US-09-326-186B-226	Sequence 226, App
2	55.3	55.5	1428	5	Sequence 1, Appl
3	54.0	54.2	1002	4	Sequence 33, Appl
4	54.0	54.2	1002	4	Sequence 33, Appl
5	54.0	54.2	1002	4	Sequence 33, Appl
6	54.0	54.2	1002	4	Sequence 33, Appl
7	54.0	54.2	1120	2	Sequence 1, Appl
8	54.0	54.2	1120	2	Sequence 1, Appl
9	54.0	54.2	1120	3	Sequence 1, Appl
10	54.0	54.2	1120	4	Sequence 22, Appl
11	54.0	54.2	1120	4	Sequence 22, Appl
12	54.0	54.2	1120	4	Sequence 22, Appl
13	54.0	54.2	1120	5	Sequence 22, Appl
14	54.0	54.2	1161	4	Sequence 24, Appl
15	54.0	54.2	1161	4	Sequence 24, Appl
16	54.0	54.2	1161	5	Sequence 24, Appl
17	53.5	53.7	972	4	Sequence 11, Appl
18	43.4	43.6	751	4	Sequence 34, Appl
19	43.4	43.6	751	4	Sequence 34, Appl
20	43.4	43.6	751	4	Sequence 34, Appl
21	33.0	33.1	1261	4	Sequence 12, Appl
22	33.0	33.1	1261	4	Sequence 12, Appl
23	33.0	33.1	1261	5	Sequence 12, Appl
24	329.6	33.1	1151	4	Sequence 3, Appl
25	329.6	33.1	1151	4	Sequence 20, Appl
26	329.6	33.1	1151	4	Sequence 20, Appl
27	329.6	33.1	1151	5	Sequence 20, Appl

28	329.6	33.1	1163	3	US-08-479-744A-22	Sequence 22, Appl
29	329.6	33.1	1163	3	US-08-280-757B-22	Sequence 22, Appl
30	225	22.6	330	3	US-08-479-744A-44	Sequence 44, Appl
31	225	22.6	330	3	US-08-280-757B-44	Sequence 44, Appl
32	159	16.0	306	3	US-08-479-744A-46	Sequence 46, Appl
33	159	16.0	306	3	US-08-280-757B-46	Sequence 46, Appl
34	101.8	10.2	210	4	US-08-205-697A-31	Sequence 31, Appl
35	101.8	10.2	210	4	US-08-702-525-31	Sequence 31, Appl
36	101.8	10.2	210	5	PCT-US95-02576-31	Sequence 31, Appl
37	59.6	6.0	195	4	US-08-205-697A-41	Sequence 41, Appl
38	59.6	6.0	195	4	US-08-702-525-41	Sequence 41, Appl
39	59.6	6.0	195	5	PCT-US95-02576-41	Sequence 41, Appl
40	37.2	3.7	7218	1	US-08-232-463-14	Sequence 14, Appl
41	33.8	3.4	2160	2	US-08-840-236-2	Sequence 2, Appl
42	33.8	3.4	2160	2	US-08-840-236-5	Sequence 5, Appl
43	33.8	3.4	2160	2	US-08-505-448A-2	Sequence 2, Appl
44	33.8	3.4	2160	2	US-08-505-448A-5	Sequence 5, Appl
45	33.6	3.4	492	4	US-09-328-111-335	Sequence 335, Appl

ALIGNMENTS

RESULT 1
US-09-326-186B-226
; Sequence 226, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Benmett, Clarence Frank
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: ISPH-03/76
; CURRENT APPLICATION NUMBER: US/09/326.186B
; PRIOR APPLICATION DATE: 1999-06-04
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-326-186B-226

Query Match 55.5%; Score 553; DB 4; Length 1424;
Best Local Similarity 75.7%; Pred. No. 1.3e-164;
Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY	4	GGCATTGTGTGACACTATGGAGTGTCTCTTGTGATGGCCCTCTGCTC	63
DB	130	GGCATTGTGTGACACTATGGAGTGTCTCTTGTGATGGCCCTCTGCTC	189
QY	64	TCTGTGTTTTCATGAGAGTGTATTTCAACAAAGTGTGAGTGTGCTTGC	123
DB	190	TCTGTGTTTTCATGAGAGTGTATTTCAACAAAGTGTGAGTGTGCTTGC	249
QY	124	CATTTCACAACTGTCAAAACATTAAGCTGTGATGTTTGGACGACGAG	183
DB	250	CAATTTCACAACTGTCAAAACATTAAGCTGTGATGTTTGGACGACGAG	309
QY	184	GATTAAGCTGTGTTGTGATGATTTCAAGAGCAAGAAACCTCAAAATGTT	243
DB	310	GAAACTGTGTTGTGATGATTTCAAGAGCAAGAAACCTCAAAATGTT	369
QY	244	AAATTAAGGCGGTGACAGCTTGAAGAGCAAGCAAGGAGCCGTCACATGTT	303
DB	370	AAATTAAGGCGGTGACAGCTTGAAGAGCAAGGAGCCGTCACATGTT	429
QY	304	CAGATCAAGCAAGGCGCATATCACTGTTTCATTATTAAGGCGCAAGGACTA	363
DB	430	CAGATCAAGCAAGGCGCTTGTATCATATCATCATCAACAAAAGCCGACAGGATG	489

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Db 1236 CTGTCATGAGAGAAATCTCAAAATATATGTCAAGAACTTACAAAGCTTCTATCAGCTTGT 1177
QY 617 CTTTTCAGTCCCTGAGACACACAAATGTGAGCGCTTTTGTGCCCTGAAACTGGAGACAC 676
Db 1176 CCTTCACAGTCCCTGAAGCAAGCATGTGAGCATTTCTGTGTGCGCAACTTGAGTCAA 1117
QY 677 TGGAGATGCTGCTCTGCTACCTTTCATATATAGATGACACACCTAAGSATTAAGA 731
Db 1116 T---GAGGCTTCCCTCCTTACCTTATATATATGAAACCAACAAGTGGAGAGAA 1065
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Search completed: October 19, 2002, 23:33:20
Job time : 157.774 secs

RESULT 13
AAZ27924/c
ID AAZ27924 standard; DNA; 840 BP.
XX
AC AAZ27924;
XX
DT 20-DEC-1999 (first entry)
XX
DE Complementary strand of canine B7-2S coding sequence.
XX
KM B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 115; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP; 214 A; 167 C; 181 G; 278 T; 0 other;

Query Match 58.5%; Score 582.2; DB 20; Length 840;
Best Local Similarity 89.4%; Pred. No. 4.2e-159;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 17 GCACATATGGAGTACACTCTCTGTGTGATGGCCCTCGTCTGTGCTTTCT 76
DB 827 GCACATATGGAGTACACTCTCTGTGTGATGGCCCTCGTCTGTGCTTTCT 768
QY 77 CCATGAGAGTCAAGCATATTTCAACAGACTGAGAACTGCATGCCATTTTAAACT 136
DB 767 CCATGAGAGTCAAGCATATTTCAACAGACTGAGAACTGCATGCCATTTTAAACT 708
QY 137 CTCAAAACATAGCCCTGAGTGTAGTATTTTGGAGAGCAAGGATTAAGCTGTTTC 196
DB 707 CTCAAAACATAGCCCTGAGTGTAGTATTTTGGAGAGCAAGGATTAAGCTGTTTC 648
QY 197 TGTATGAGATATTCAGAGCAAAAGAGACCTCAAAATTTTCATGCTCAATATTAAGGCC 256
DB 647 TGTATGAGATATTCAGAGCAAAAGAGACCTCAAAATTTTCATGCTCAATATTAAGGCC 588
QY 257 GTACAAAGCTTTGACAAAGCAACTGACCTGAGACTCCACAATGTTGATCAAGGACA 316
DB 587 GTACAAAGCTTTGACAAAGCAACTGACCTGAGACTCCACAATGTTGATCAAGGACA 528
QY 317 AGGGACATATCTACTGTTTCATTTAATAAGGCGCCCAAGGACTAGTCCCATGACCC 376

DB 527 AGGGCTTGTATCAATGTTTCCTTCATCAATAAGGCGCCCAAGGACTGTTCCATGACCC 468
QY 377 AATGAGTTCGTACCTATCACTGCTGTACTACATCAACCGAATTAAGTACTT 436
DB 467 AGATGAATTTGACCTATCACTGCTGTACTACATCAACCGAATTAAGTACTT 408
QY 437 CTAATAGAACAAAATTTCTGGCATCATTAATTTGACCTGCTCATCTATCAAGGTTACC 496
DB 407 CTAATAGAACAAAATTTCTGGCATCATTAATTTGACCTGCTCATCTATCAAGGTTACC 348
QY 497 CAGAACCTAAGAGATGATTTTCACTCAAACTGAGATTTCACTACATGATGATA 556
DB 347 CAGAACCTAAGAGATGATTTTGGTAAAACCGGAATTCAGTACATGATGATA 288
QY 557 CTGTCTATGAGAAATCTCAAAATATGATGACAGAACTGACAACTGTTCTATGAGCTTGC 616
DB 287 CTGTCTATGAGAAATCTCAAAATATGATGACAGAACTGACAACTGTTCTATGAGCTTGT 228
QY 617 CTTTTCAGTCCCTGAAGCAGACAAATGTGAGCGCTTTTGTGCCCTGAACCTGGAGACAC 676
DB 227 CTTTTCAGTCCCTGAAGCAGACAAATGTGAGCGCTTTTGTGCCCTGAACCTGGAGACAC 168
QY 677 TGGAGATCTGCTCTCCCTACCTTTCATATAGATGACAAACCTAAGGATTAAGA 731
DB 167 T--GAAGCTTCCTCCCTACCTTATATATAGAAACCAAAAGTGGAGAGAAA 116

RESULT 14
AAZ27921
ID AAZ27921 standard; DNA; 1795 BP.
XX
AC AAZ27921;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein encoding DNA.
XX
KM B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
DR P-PSDB; AA41078.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 109-111; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,

|||||
Db 394 TAGAGTCTGACCTATCAGAGCTTGCTTAACCTGCAACCTGAAATTAACCTACTACTACTA 453
Oy 440 ATAGAGACAGAAATTTGCGATCATTAATTTGACCTGGCTCATTAAGGTTACCCAG 499
Db 454 ATCAGACAGAAATTTCTG---TCATTAATTTTACTGCTCATCTACACAGAGCTACCCAG 510
Oy 500 AACCTAGAGAGATGATTTTTCAGCTAATACCTAGAAATTTCACTAAGTATGATAGT 559
Db 511 AACCCAGAGAGATGATGATTTGCTAATATACAGAAATTTCAACCTAGAGCTAGCTGCTG 570
Oy 560 TCATGAGAGAAATTTCAAAATATATGACAGAACTGACAACTTTCTATAGCTTGCTT 619
Db 571 ACATGAGAGAAATTTCAAAATATATACATCAGGAACTGTACAAATGATATCAATCAGGGGTCTC 630
Oy 620 TTTCAAGTCCCTGAAAGACACATGTGAGGCTTTTGTGCCCTGAAACGTGGAGACACTGG 679
Db 631 TTCCCATCTCCCTCCGAGACAAATGTGAGCATGCTGTGTCTGCAACTTGAGCCAGCA 690
Oy 680 AGA---TGCTGCTCTCCCTACCTTTCAATATATAGATGACACAACTAAGATATAAGACCTG 736
Db 691 AGACACTGCTTTTCTCCCTACCTGTAATATATGATGCAAGGCTACCTGAGCAACCCCTG 750
Oy 737 AACAGGCACTTCTCTGTGATTCGCGCTGTACTGTATGTTTGTGTTTGTGGGA 796
Db 751 TCCGAGACACATCTCTGATTTGAGCTCTAATGTAACATGTGCTGTGTGTGGGA 810
Oy 797 TGGTGTCTTTTAAACACTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
Db 811 TGGTGTCTTTTAAACACTAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
Oy 857 ---GTGAAACATCAAAAGGAG 913
Db 871 GTGGTGAACCATCAAAATGAACAGGAGGCGAGTGAACCAACTAAGAAAGAGAGAGAGAGAG 926
Oy 914 ACCAGTACCTGAGAGATCTGATGAAGCCAGTGT---TATTAACTTTTGAAGAGAGCT 970
Db 927 --GAAGTCATTAACGATCTGATGATGCCAGTGTGATGTTTAAATTTTAAAGAGAGCT 984
Oy 971 CAGGGACAAAAGTACTACACATTTT 996
Db 985 CAGATGACAAACGACTACTACAGATTTT 1010

RESULT 12
AAZ27923
ID AAZ27923 standard; DNA: 840 BP.
XX
AC AAZ27923;
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein coding sequence.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN MO9947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX

DR WPI: 1999-571822/48.
DR P-PSDB: AAY41078.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX
PS Claim 1: Page 114; 148bp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP: 278 A; 181 C; 167 G; 214 T; 0 other:
XX
Query Match 58.5%; Score 582.2; DB 20; Length 840;
Best Local Similarity 89.4%; Pred. No 4.2e-159;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
Oy 17 GCATATGAGAGTGAAGTCAACATCTCTGTGATGGCCCTGCTCTGTGTGTTCTT 76
Db 14 GCATATGAGAACTAATATACATTTCTTTGTGATGACCTCTGCTCTATGTGTGCTT 73
Oy 77 CCATGAGAGTCAAGCATATTTTCAACAAGCTGGAAGACTGCCATGCGATTTTACAAC 136
Db 74 CCATGAGAGAGTCAAGCATATTTTCAACAAGCTGGAAGACTGCCATGCGATTTTACA 133
Oy 137 CTCAAACATTAAGCTGTGATGAGCTGTATATTTTGGCAGGACCAAGATTAAGCTGTT 196
Db 134 CTCAAACATTAAGCTGTGATGAGCTGTATATTTTGGCAGGACCAAGATTAAGCTGTT 193
Oy 197 TGTATGATATTTCAAGGAGCAAGAGACCTCAAAATTTTCAATATATTAAGGCC 256
Db 194 TGTACGAGCTATACAGGCAAGAGAACCTCAAAATTTTCAATATATTAAGGCC 253
Oy 257 GTACAGCTTTGACAAAGCAAGCAAGCTGAGACCTGAGACCTCAATGTTCAAGTAAAGSAC 316
Db 254 GCACAGCTTTGACAAAGCAAGCAATTTGACCTGAGACCTCAATATTTCAAGTAAAGSAC 313
Oy 317 AGGCGACATATCACTGTTTCATTTATTAAGGGCCCAAGAGACTAGTCCATGACCC 376
Db 314 AGGCGCTGTATCAATGTTTCTTCATATCAATTAAGGCCCAAGAGACTGTTCCATGACCC 373
Oy 377 AATGAGTTCTGACCTATCAAGCTGCTGCTCACTCAAGTCAAGTCAAGTCAAGTCAAGT 436
Db 374 AGATGAATTTCTGACCTATCAAGTGTGCTGCTCAAGTCAAGTCAAGTCAAGTCAAGT 433
Oy 437 CTATATAGACAGAAATTTGCGATCATTAATTTGACCTGCTCATATATCAAGTCAAGT 496
Db 434 CTATATAGACAGAAATTTGCGATCATTAATTTGACCTGCTCATATATCAAGTCAAGT 493
Oy 497 CAGAACCTAAGAGATGATTTTCAAGCTAACAAGTGAATTCAGTCAAGTCAAGTCAAGT 556
Db 494 CAGAACCCAGAGAGATGATTTTGGTAAACCCGAGATTCAGTCAAGTCAAGTCAAGT 553
Oy 557 CTGTCATGAGAAATTTCAAAATATATGTCAGACAGTCAAGTCAAGTCAAGTCAAGT 616
Db 554 CTGTCATGAGAAATTTCAAAATATATGTCAGACAGTCAAGTCAAGTCAAGTCAAGT 613
Oy 617 CTTTTCAGTCCCTGAAGCAGACATGTGAGCTCTTTTGTGCCCTGAAAGTGAAGAC 676
Db 614 CTTTTCAGTCCCTGAAGCAGACATGTGAGCTCTTTTGTGCCCTGAAAGTGAAGAC 673
Oy 677 TGGAGATGCTGCTCTCACTTTCAATATATGATGATGATGATGATGATGATGAT 731
Db 674 T---GAAGCTTCCCTCCCTACCTTATATATATGAAACCAACAAAGTGAAGAGAA 725

D	b	1699	TGTCAGGCTATACAGAGGCCAAGAAGAACCCCTCAAAATGTTCATGCACAAGTATAAGGCC	1640
O	y	257	GTAACAACCTTTGACACAGGAACAACCTGGACCCCTGAGACTCCACATGTTCAATGATCAAGACA	316
D	b	1639	GCAACACCTTGACAAAAGCAAAATTGGACCCCTGAGACTCCATTAATTCATGATCAAGACA	1580
O	y	317	AGGCGCATATATACACTGTTTCATTCATTAATAAAGGGCCCCAABAGACTAGTCCCATGACC	376
D	b	1579	AGGGCTTGATCATTGTTTGGTTCATCATATAAAGGCCCAABAGACTCGTTCATGACC	1520
O	y	377	AAATGACTTGACCTATACAGTGCCTGGCTGAACCTGATCACACCTGAATTAACGTAACCT	436
D	b	1519	AGATGATTTGTGACCTATACAGTCTGTTGCTAAGCTGAGTCAACCTGAATAATAGTAACCT	1460
O	y	437	CTATTAAACAGAAAATTCGSGATATATAATTTGACCTGCTCATCTATACAAAGTTACC	496
D	b	1459	CTAATTAACAGAAAATTCGSGATATATAATTTGACCTGCTCATCTATACAAAGTTACC	1400
O	y	497	CAGAACCTAAGAGAGATATTTTCACCTTAAGACCTGAGATTAACACTACTAAGTAGTA	556
D	b	1399	CAGAACCCAAGAGATGATTTTTTGGTAAAAACGAGAAATTCAGTACTGTAAGTAGTA	1340
O	y	557	CTGTCATGAAGAATTCGCAAAATATGTGACAGACTGTACAAAGTTCTATACAGTTGC	616
D	b	1339	CTGTCATGAAGAATTCGCAAAATATGTGACAGAACTGACAAAGCTTCTATACAGCTTGT	1280
O	y	617	CTTTTCAGTCCCGAAGCAGACATGTAGAGCTTTTGTGSCCTGAACAGTGAGACAC	676
D	b	1279	CTTTCAGTCCCGAAGCAGAAAGATGTAGAGCTTCTGTGTCTCTGCAACTGTAGTCAA	1220
O	y	677	TGAGATGCTGCTCTCCCTACCTTTCAATATAGANTGCACAACTAAGATAAAGACCTG	736
D	b	1219	T---GAAGCTTCCCTCCCTCACTTATAATATGATGCACA---TAGAAACCCACCCCTG	1166
O	y	737	AACAAGCCACTTCCCTCGATGGCGCTGACCTGTATGTTGTTGTTTGTGGGA	796
D	b	1165	ATGAGAACCAATCTGTGATTTGCAGCTCTGTTTAATGTTGGTCAATTTGTGTGGGA	1106
O	y	797	TGTTGCTTTTAAACACTAAGGAAAAGAGAAGAACAGCCTGAGCCCTCTCATGAT	856
D	b	1105	TGGTGTCTTTCTTAACACTAAGGAAAAGAGAAGAACAGCCTGAGCCCTCTCATGAT	1046
O	y	857	GTGAACCATCAAAAAGSAGAGAAGAAGACCAACAGACCAAGAAAGATACATACC	916
D	b	1045	GTGAACCATCAAAAAGTGAAGAAGAAAGTGAAGACCAAGAAAGAAAGTACGATACC	986
O	y	917	ACGATCTGAGAGATGTGAAGAAGCCAGTGTATTAATTTTGAAGACAGCTCAGGCG	976
D	b	985	ATGAAGCGAAAGATGTGAAGAAGCCAGTGTATTAATTTTGAAGACAGCTCAGGCG	926
O	y	977	ACAAAGTACTACATTTT 996	
D	b	925	ACAACAGTACTACACAGTTT 906	
RESULT_11				
ID	AAAA9661	standard; cDNA; 1050 BP.		
XX	AA			
AC	AA			
DT	25-SEP-2000	(first entry)		
DE	pig costimulatory molecule CD86 (B7-2) cDNA.			
KW	Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;			
KM	xenotransplantation; organ transplant; vaccine; ss.			
OS	Sus scrofa.			
XX				
FH	key	Location/Qualifiers		
FT	CDS	36..1013		
FT	*	/*tag= a		

[illegible]

50 Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2.

Db 20 ACAACAGTACTACACAGTTT 1

ID AA227913 standard; DNA; 1897 BP.

AC AAZ27913;

DT 20-DEC-1999 (first entry)

DE Canine B7-2 protein encoding DNA.

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.

PN W09947558-A2.

PD 23-SEP-1999.

PF 19-MAR-1999;

PR 19-MAR-1998; 98US-0078765.

[illegible]

XX 117

XX 7
C
H
C
7
C
C
H
H
C
C
C

DR P-PSDB: AAY41076.

AA
PT
New isolated B7 and

FI Creating, e.g. autoc
XX

CLALL 1; Page 31-33
XX

CC encoding nucleic acid

CC expressed by standard
CC and the encoded prot

CC e.g. autoimmune disease

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Db 963 GAAGAGTACCTACCTACCTAGAGAGATGTGTAAGCCCACTGTGTTAACAATTTTG 1022
Qy 961 AAGACAGCCTCAGCGCAAAAGT 984
    |||||
Db 1023 AAGACAGCCTCAGCGCAAAAT 1046

RESULT 7
AA227915
ID AA227915 standard; DNA: 987 BP.
AC AA227915;
AT 20-DEC-1999 (first entry)
DE Canine B7-2 protein coding sequence.
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
XX MO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
XX
XX P-PSDB; AAY41076.
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1; Page 102-103; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match 78.88; Score 784.8; DB 20; Length 987;
Best Local Similarity 89.08; Pred. No. 5.2e-218;
Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

Qy 17 GCACTATGAGCAGTCACTCTCTGTGATGCGCCCTCCCTGCTGCTGCTGCTTCTT 76
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14 GCACATATGAACTCAATTAACATCTCTCTTGTGATGACCTCTCTCTATGCTGCTT 73

Qy 77 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGAGAACTGCCATGCTTACAAACT 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 74 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGAGAACTGCCATGCTTACAAAT 133

Qy 137 CTCAAAACATTAAGCCTGAGAGCTGTGATATTTTGGCAGGACCAAGATTAAGCTGTT 196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 134 CTCAAAACATTAAGCCTGAGAGCTGTGATATTTTGGCAGGACCAAGATTAAGCTGTT 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 197 TGTATGATATTTAGAGGGAAGAGAACCTCAAAATGTTCAATATTAAGGCC 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 194 TGTACAGCTATACAGAGGAAGAGAACCTCAAAATGTTCAATTCGAAGTATAAGGCC 253
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257 GTACAACTTTGACAAAGAACTGGACCTGAGACTCCCAATGTTTCAGATTAAGACA 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 254 GCACAACTTTGACAAAGAACTGGACCTGAGACTCCCAATTAATTCAGATTAAGACA 313
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 317 AGGCACATATTCAGCTGTTTATTCATATTAAGAGGCCCAAGAGACTAGTCCATGACC 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 314 AGGCCTTGATCAATGTTTGGTTCATATTAAGAGGCCCAAGAGACTGTTCCATGACC 373
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 377 AATGAGTCTGACCTATTCAGCTGCTTGTCTTAAGTCAAGTCAAGTGAATTAAGTACT 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 374 AGATGAATTCGACCTATTCAGCTGCTTGTCTTAAGTCAAGTGAATTAAGTACT 433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 437 CTATATACAGAAATTCGACATATTAATTTGACCTGCTGCTATATTAAGTACTTACC 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 434 CTATATACAGAAATTCGACATATTAATTTGACCTGCTGCTATATTAAGTACTTACC 493
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 497 CAGAACCTAAGAGATGATTTTTCAGCTAACACTGAGAAATTCAGTAAATGATGATA 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 494 CAGAACCTAAGAGATGATTTTTCAGCTAACACTGAGAAATTCAGTAAATGATGATA 553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 557 CTGTCAATGAAGAAATTCAGAAATATGTCAGAGACTGTACAAAGTTCATCAGCTTGC 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 554 CTGTCAATGAAGAAATTCAGAAATATGTCAGAGACTGTACAAAGTTCATCAGCTTGT 613
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 617 CTTTTCAGTCCCTGAAGCAGCAATGTGAGCGTCTTTGTGCGCGGAACGAGAGACAG 676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 614 CTTTTCAGTCCCTGAAGCAGCAATGTGAGCGTCTTTGTGCGCGGAACGAGAGACAG 673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 677 TGAAGATGCTGCTCCCTACCTTCAATATAGATGACAGACCTAAGATTAAGACCTG 736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 674 T---GAAGCTTCCCTCCCTCAATATATATAGATGACACA--TAGAAGACCAAGCCCTG 727
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 737 AACAAGGCCACTCTCTGATTCGCGTGTACTGTATGTTTGTGTTTGTGAGGA 796
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 728 ATGAGACACATCTCTGATTCGCGTGTACTGTATGTTTGTGTTTGTGAGGA 787
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 797 TGGTGTCTTTAAACATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 856
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 788 TGGTGTCTTTTCAACACTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 847
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 857 GTGAACCATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCAC 916
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 848 GTGAACCATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCAC 907
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 917 AGCTACCTGAGAGATGTGATGAAGCCAGTGTATTAATTTTGAAGAGAGAGAGAGAG 976
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 908 ATGAACGGGAAGATGTGATGAAGCCAGTGTGTTAACAATTCGAGAGAGAGAGAGAG 967
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 977 ACAAAAGTACTACACATTTT 996
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 968 ACAAGACTACTACAGTTT 987
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
AA227916/c
ID AA227916 standard; DNA: 987 BP.
AC AA227916;
AT 20-DEC-1999 (first entry)
DE Complementary strand of canine B7-2 coding sequence.
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
XX
XX MO9947558-A2.
XX
```

DB	1023	AAAGCAGCCTCAGGGGACAAAAT 1046
RESULT 6		
AA234785		
AC	AA234785	standard; cDNA; 1080 BP.
XX		
XX	15-FEB-2000	(first entry)
XX		
DE	Cat CD86 (B7-2)	cDNA.
XX		
KM	CD86; B7-2; ligand; cat; vaccine; feline immunodeficiency virus;	
KM	FTV; feline leukemia virus; feline infectious peritonitis virus;	
KM	feline panleukopenia virus; feline calicivirus; feline reovirus-3;	
KM	feline rotavirus; feline coronavirus; feline syncytial virus;	
KM	feline sarcoma virus; feline herpesvirus; feline Borna disease;	
KM	rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;	
KM	parasite; autoimmune disease; transplant rejection; therapy; ss.	
XX		
OS	Felis domesticus.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	63..1055
FT		/*tag= a
XX		
PM	W09957271-A2.	
XX		
PD	11-NOV-1999.	
XX		
XX	30-APR-1999;	99WO-US09502.
PF	01-MAY-1998;	98US-0071659.
XX		
PA	(TEXAS) TEXAS A & M SYSTEM.	
XX		
XX	Collison EM, Hash SM, Choi I;	
DR	WPI: 2000-052972/04.	
XX	P-PSDB: AAY32278.	
XX		
PT	Novel feline proteins used to produce feline vaccines which prevent	
PT	infectious disease or to promote growth in homologous or heterologous	
PT	species -	
XX		
PS	Claim 6; Fig 3A; 186pp; English.	
XX		
CC	This is the nucleotide sequence of cDNA encoding feline CD86	
CC	(B7-2) ligand (see AAY32278). It was obtained following RT-PCR of	
CC	peripheral blood mononuclear cell mRNA and RACE-PCR. A vector	
CC	comprising nucleic acid encoding feline CD86 ligand or feline	
CC	soluble CD80 ligand is designated PST-2#19-2/011298 (ATCC 209821).	
CC	The coexpression of CD86 with the costimulatory molecules CD28 (see	
CC	AAY32278) and a tumor antigen or an antigen from a pathogenic	
CC	organism has the ability to activate or enhance activation of	
CC	T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has	
CC	the ability to regulate activation of T-lymphocytes. The invention	
CC	provides isolated nucleic acids encoding feline CD86 ligand,	
CC	feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4	
CC	(CD152) receptor, as well as vectors comprising the nucleic acids,	
CC	and polypeptides encoded by the nucleic acids. It also provides,	
CC	vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and	
CC	further comprising immunogens derived from pathogens, especially	
CC	feline immunodeficiency virus (FIV), feline leukemia virus,	
CC	feline infectious peritonitis virus, feline panleukopenia virus,	
CC	feline calicivirus, feline reovirus-3, feline rotavirus, feline	
CC	coronavirus, feline syncytial virus, feline sarcoma virus, feline	
CC	herpesvirus, feline Borna disease virus, rabies virus, chlamydia,	
CC	Toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial	
CC	pathogen, or parasite (all claimed). Vaccines capable of	
CC	enhancing an immune response (all claimed) and vaccines capable of suppressing	

Query Match	Best Local Similarity	98.3%	Score 979.2	DB 21	Length 1080
Matches 981	Conservative	99.7%	Prod. No. 1.5e-274	Mismatches 3	Indels 0
					Gaps 0
1	ATGGGCATTTTGAGACGACATATGAGGAGCTGAGTGCACACTCTCCTTGATGAGCCCTCCG	60			
63	ATGGCATTTTGAGACGACATATGAGGAGCTGAGTGCACACTCTCCTTGATGAGCCCTCCG	122			
61	CTCTCTGCTGTTCTTCCATGAGAGTCAAGCATATTTCAACAAGACTGGAAACTGCCA	120			
123	CTCTCTGCTGTTCTTCCATGAGAGTCAAGCATATTTCAACAAGACTGGAAACTGCCA	182			
121	TGCGCATTTTACAAACCTCTGAAACATATTAACCCGTGATGAGCTGTAATTTTGGCAGAC	180			
183	TGCGCATTTTACAAACCTCTGAAACATATTAACCCGTGATGAGCTGTAATTTTGGCAGAC	242			
181	CAGGATTAAGCTGGTCTGTATGAGATATTTCAGAGGCAAGAGAACCCCTCAAAATGTTCA	240			
243	CAGGATTAAGCTGGTCTGTATGAGATATTTCAGAGGCAAGAGAACCCCTCAAAATGTTCA	302			
241	CTCAATATTAAGGCGCTCAAGCTTTGCAAGGCAACCTGGACCCCTGAGCTCCACAT	300			
303	CTCAATATTAAGGCGCTCAAGCTTTGCAAGGCAACCTGGACCCCTGAGCTCCACAT	362			
301	GTTTCAGTCAAGGACAAAGGCGACATATCACTGTTTCATTATTAATTAAGGCGCCAAAGA	360			
363	GTTTCAGTCAAGGACAAAGGCGACATATCACTGTTTCATTATTAATTAAGGCGCCAAAGA	422			
361	CTAGTTCCTCATGACCAAAATGATTTGACCTATACAGTCTTGCTTAACCTTCACTCAACT	420			
423	CTAGTTCCTCATGACCAAAATGATTTGACCTATACAGTCTTGCTTAACCTTCACTCAACT	482			
421	GAAATACAGTAACTCTATAGAACAGAGAAATTCGGCATCTAATAATTTGACCTGCTCA	480			
483	GAAATACAGTAACTCTATAGAACAGAGAAATTCGGCATCTAATAATTTGACCTGCTCA	542			
481	TCTATACAAAGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCA	540			
543	TCTATACAAAGTTACCCAGAACCTAAGAGATGATTTTCAGCTAAACACTGAGAAATTCA	602			
541	ACTACATAGATGATATCTGTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACAC	600			
603	ACTACATAGATGATATCTGTCATGAGAAATCTCAAAATATATGTGACAGAACTGTACAC	662			
601	GTTTCTATCAGCTTGCCCTTTTTCAGTCCCTGAGGACACAAATGTAGAGCGCTCTTTTGCC	660			
663	GTTTCTATCAGCTTGCCCTTTTTCAGTCCCTGAGGACACAAATGTAGAGCGCTCTTTTGCC	722			
661	CTGAACTGAGACACTGAGATGCTGCTCCCTCACTTCAATATATGATGACAAACCT	720			
723	CTGAACTGAGACACTGAGATGCTGCTCCCTCACTTCAATATATGATGACAAACCT	782			
721	AAGGATTAAGACCTCTGAGAACAGGCACTTCTCTGATTTGGGCTCTACTTGTATGTTT	780			
783	AAGGATTAAGACCTCTGAGAACAGGCACTTCTCTGATTTGGGCTCTACTTGTATGTTT	842			
781	GTTGTTTTTTTGGGATGGTGTCTTTTAAACACTTAAGGAAAGGAAAGGAGAGCGCT	840			
843	GTTGTTTTTTTGGGATGGTGTCTTTTAAACACTTAAGGAAAGGAAAGGAGAGCGCT	902			
841	GCGCCCTCTCATAAATGTGAACCATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	900			
903	GCGCCCTCTCATAAATGTGAACCATCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG	962			
901	GAAAGGTACCATCAAGTACTGAGAGATCTGATGAGGCCAGTGTATTAACATTTTG	960			

OY	421	GAAATACACTACTACTCTCTAATATGAACAGAAATTCCTGGCATCATTAATATGACCTGCTCA	480
Db	599	GAAATACACTACTACTCTCTAATATGAACAGAAATTCCTGGCATCATTAATATGACCTGCTCA	658
OY	481	TCCTATACAAAGTTATACCAGAACCTTAAGAGATATTTTTCAGCTTAACACTGAGAAATTC	540
Db	659	TCCTATACAAAGTTATACCAGAACCTTAAGAGATATTTTTCAGCTTAACACTGAGAAATTC	718
OY	541	ACTATCTAAGTATATATCTACTGTCATGAAGAAATCTCAAAATTAATGTGTACAGAACTGTACAC	600
Db	719	ACTATCTAAGTATATATCTACTGTCATGAAGAAATCTCAAAATTAATGTGTACAGAACTGTACAC	778
OY	601	GTTTCTATCTACGCTTGGCTTTTTCAGTCCCTGGAAGCACACAAATGTGAGCGCTTTTGTGGC	660
Db	779	GTTTCTATCTACGCTTGGCTTTTTCAGTCCCTGGAAGCACACAAATGTGAGCGCTTTTGTGGC	838
OY	661	CTGAACCTGAGACACTGTGAGATGCTGCTCTCCCTACCTTTCAATATATGATGCACAACT	720
Db	839	CTGAACCTGAGACACTGTGAGATGCTGCTCTCCCTACCTTTCAATATATGATGCACAACT	898
OY	721	AAGATATTAAGCCCTGAAACAAGGCCACTCTCTGTGATTTGGGGCTGTACTTGTATATGTT	780
Db	899	AAGATATTAAGCCCTGAAACAAGGCCACTCTCTGTGATTTGGGGCTGTACTTGTATATGTT	958
OY	781	GTTGTTTTTTGTGGAGTGTGTCCTTTAAACACTAAGGAAAGAGAAAGAACGACGCT	840
Db	959	GTTGTTTTTTGTGGAGTGTGTCCTTTAAACACTAAGGAAAGAGAAAGAACGACGCT	1018
OY	841	GGCCCCCTCATGATGTGTGAACCAATCAAAAGGAGACAGAAAGACAGCAACGACCAAC	900
Db	1019	GGCCCCCTCATGATGTGTGAACCAATCAAAAGGAGAGAAAGAGACAGCAACGACCAAC	1078
OY	901	GAAAGAGTACCATACCACTGATCCCTGAGAGATCTGATGAAGGCCAGTGTATTAACATTTTG	960
Db	1079	GAAAGAGTACCATACCACTGATCCCTGAGAGATCTGATGAAGGCCAGTGTATTAACATTTTG	1138
OY	961	AAGACAGCCTCTGAGCGCGACAAAAGTACTACATTTT	996
Db	1139	AAGACAGCCTCTGAGCGCGACAAAAGTACTACATTTT	1174
RESULT 4			
AAZ27930/C			
ID	AAZ27930 standard, DNA: 2830 BP.		
XX			
AC	AAZ27930;		
XX			
DT	20-DEC-1999 (first entry)		
XX			
DE	Feline B7-2 gene complementary DNA sequence.		
XX			
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;		
KM	allergic reaction; infectious disease; tumor development; feline;		
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.		
OS			
XX	Felis catus.		
XX			
PN	W09947558-A2.		
XX			
PD	23-SEP-1999.		
XX			
PF	19-MAR-1999; 99WO-US06187.		
XX			
PR	19-MAR-1998; 98US-0078765.		
PR	17-APR-1998; 98US-0062597.		
XX			
PA	(HESK-) HESKA CORP.		
XX			
PI	Sim G, Yang S, Sellins KS;		
XX			
DR	WPI, 1999-571822/48.		
XX			
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for		

PT	treating e.g. autoimmune and atopic diseases
XX	
PS	Claim 1; Page 121-123; 148pp; English.
CC	The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC	encoding nucleic acid molecules from dogs and cats. The proteins can be
CC	expressed by standard recombinant methodology. The nucleic acid molecules
CC	and the encoded proteins can be used for preventing or treating diseases,
CC	e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC	development, graft rejection, inflammation, arthritic and atopic diseases
CC	such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC	cats, cattle, sheep or pets. The products can also be used for detection,
CC	diagnosis and drug screening.
XX	
SQ	Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other;
Query Match	100.0%; Score 996; DB 279; Length 2830;
Best Local Similarity	100.0%; Pred. No. 3,1e-279;
Matches 996; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGGCATTGTGACAGCACTATGGAGACTGCACACTCTCTTGATGGCCCCCTCG 60
DB	2652 ATGGGCATTGTGACAGCACATAAGGAGACTGCACACTCTCTTGATGGCCCCCTCG 2593
OY	61 CTCTCGTGTTTCCTCATGAAGTCAAGCATATTTAAACAAGCTGGAAACTGCCA 120
DB	2592 CTCCTGGTGTTCTTCATGTAAGTCAAGCATATTTTCAAACAAGCTGGAAACTGCCA 2533
OY	121 TGCATTATTAACAACCTCTCAAAAACATAACCCTGGATGACCTGGTAGTATTTGGCAGAGC 180
DB	2532 TGCATTATTAACAACCTCTCAAAAACATAACCCTGGATGACCTGGTAGTATTTGGCAGAGC 2473
OY	181 CAGGATAGCTGTCTGTATGATATATTCAGAGCCAAGAAGAACCCCTCAAAATGTTCA 240
DB	2472 CAGGATAAACCTGTCTGTATGATATATTCAGAGCCAAGAAGAACCCCTCAAAATGTTCA 2413
OY	241 CTCAAATATAAGGGCGGTCAAGCTTGGACAAGGAACTGGGCCCTGGAGCTCCCAAT 300
DB	2412 CTCAAATATAAGGGCGGTCAAGCTTGGACAAGGAACTGGGCCCTGGAGCTCCCAAT 2353
OY	301 GTTTCAGATTAAGGACAAGGGCAATATVCACTGTTTCATTATTAATAAGGGCCCAANA 360
DB	2352 GTTTCAGATTAAGGACAAGGGCAATATVCACTGTTTCATTATTAATAAGGGCCCAANA 2293
OY	361 CTAGTTCCCATGCAACCAATAGTGTGACCTATACAGTGCTTGCTATCTCACTCAACCT 420
DB	2292 CTAGTTCCCATGCAACCAATAGTGTGACCTATACAGTGCTTGCTATCTCACTCAACCT 2233
OY	421 GAATATACAGTAACTCTATATAGAACAGAAAAATTCGGCATCATTAATTTGACCTGCTCA 480
DB	2232 GAATATACAGTAACTCTATATAGAACAGAAAAATTCGGCATCATTAATTTGACCTGCTCA 2173
OY	481 TCTATCAAGGTTACCCAGAACCTAAGAGATGTATTTTACGCTAAACACTGGAATTTCA 540
DB	2172 TCTATCAAGGTTACCCAGAACCTAAGAGATGTATTTTACGCTAAACACTGGAATTTCA 2113
OY	541 ACTACTAAGTATGATCTGTCATGAAGAATCTCAAAATPATGTGACAGAACTGTCACAC 600
DB	2112 ACTACTAAGTATGATCTGTCATGAAGAATCTCAAAATPATGTGACAGAACTGTCACAC 2053
OY	601 GTTTCATCAGCTTGCCCTTTTCAGTCCCTGAAGCACACATGTGAGCGCTCTTTGTGCC 660
DB	2052 GTTTCATCAGCTTGCCCTTTTCAGTCCCTGAAGCACACATGTGAGCGCTCTTTGTGCC 1993
OY	661 CTGAAACTGGAGCACTGGAGATGCTGCTCCCTCACTTCAATATAGATGCAACAACCT 720
DB	1992 CTGAAACTGGAGCACTGGAGATGCTGCTCCCTCACTTCAATATAGATGCAACAACCT 1933
OY	721 AAGGATAAAGACCCCTGACAAAGSCACTTCTCTGATTGGCGCTCTACTTGTAAATGTTT 780
DB	1932 AAGGATAAAGACCCCTGACAAAGSCACTTCTCTGATTGGCGCTCTACTTGTAAATGTTT 1873
OY	781 GTTGTGTTTTTGTGGATGCTGCTTTTAAACAATAAGGAAAAAGAAAGAAAGACGCT 840

```
QY 61 CTCCTGCTGTTCTTCCATGAGAGTCGACGATATTTTCAAGAGAGTGGAGAACTGCCA 120
Db 936 CTCCTGCTGTTCTTCCATGAGAGTCGACGATATTTTCAAGAGAGTGGAGAACTGCCA 877
QY 121 TGGCATTATTAACACCTGCAAAACATTAAGCCTGGATAGCTGTGATATTTTGGCAGAC 180
Db 876 TGGCATTATTAACACCTGCAAAACATTAAGCCTGGATAGCTGTGATATTTTGGCAGAC 817
QY 181 CAGGATAGAGTGTCTGTATGAGATATTCAGAGGCAAGAGAACCTCAAAATGTTTCAT 240
Db 816 CAGGATAGAGTGTCTGTATGAGATATTCAGAGGCAAGAGAACCTCAAAATGTTTCAT 757
QY 241 CTCAAATATTAAGGCGCGTACAGCTTTGACAGAGACAACTGGACCTGAGACTCCACAT 300
Db 756 CTCAAATATTAAGGCGCGTACAGCTTTGACAGAGACAACTGGACCTGAGACTCCACAT 697
QY 301 GTTACAGATCAAGAGGAGGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 360
Db 696 GTTACAGATCAAGAGGAGGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 637
QY 361 CTAGTCCCATGACCAAAATGAGTTTCAGACTATCAGTGTTCATCATTAATAAGGGCCCAAGGA 420
Db 636 CTAGTCCCATGACCAAAATGAGTTTCAGACTATCAGTGTTCATCATTAATAAGGGCCCAAGGA 577
QY 421 GAAATACAGTACTTCTAATAGACGAAATTTCTGGCATCATTAATTTGACCTGCTCA 480
Db 576 GAAATACAGTACTTCTAATAGACGAAATTTCTGGCATCATTAATTTGACCTGCTCA 517
QY 481 TCTATCAAGGTTACCCAGACCTTAAGAGATGATATTTAGTAAACGTCAGCATTTCA 540
Db 516 TCTATCAAGGTTACCCAGACCTTAAGAGATGATATTTAGTAAACGTCAGCATTTCA 457
QY 541 ACTATCAAGTATGATGATGTCATGAAGAAATCTCAAAATATGATGACAGAACTGTACAC 600
Db 456 ACTATCAAGTATGATGATGTCATGAAGAAATCTCAAAATATGATGACAGAACTGTACAC 397
QY 601 GTTTCATCAAGTGTGCTTTTCAAGTCCGACAGACAAATGACGCTTTTGTGCTC 660
Db 396 GTTTCATCAAGTGTGCTTTTCAAGTCCGACAGACAAATGACGCTTTTGTGCTC 337
QY 661 CTGAAACGAGACACGAGATGCTCTTCAACCTTCAATATGATGACAACTG 720
Db 336 CTGAAACGAGACACGAGATGCTCTTCAACCTTCAATATGATGACAACTG 277
QY 721 AAGGATTAACACCTGACAAAGGCGACTTCTGATTTGCGGCTGTACTGTATGTTT 780
Db 276 AAGGATTAACACCTGACAAAGGCGACTTCTGATTTGCGGCTGTACTGTATGTTT 217
QY 781 GTTGTCTTGTGGATGCTCTTAAACACTAAGGAAAGGAAAGGAGGCGCT 840
Db 216 GTTGTCTTGTGGATGCTCTTAAACACTAAGGAAAGGAAAGGAGGCGCT 157
QY 841 GGGCCCTCTCATGATGTAAGCAACATCAAAAGGAGAGAAAGAGCAAGACGACCAAC 900
Db 156 GGGCCCTCTCATGATGTAAGCAACATCAAAAGGAGAGAAAGAGCAAGACGACCAAC 97
QY 901 GAAAGATGACATACACAGTACTGAGATGATGATGAAAGCCAGTGTATTACATTTTG 960
Db 96 GAAAGATGACATACACAGTACTGAGATGATGATGAAAGCCAGTGTATTACATTTTG 37
QY 961 AAGACAGCCTCAGGCGACAAAGTACTACATTTT 996
Db 36 AAGACAGCCTCAGGCGACAAAGTACTACATTTT 1
RESULT 3
AA227929
ID AA227929 standard; DNA; 2830 BP.
AC AA227929;
XX
XX 20-DEC-1999 (first entry)
XX
```

```
DE Feline B7-2 protein encoding DNA.
XX
XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; feline;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Fells catus.
XX
XX MO9947558-A2.
XX
XX 23-SEP-1999.
XX
XX 19-MAR-1999; 99WO-US06187.
XX
XX 19-MAR-1998; 98US-0078765.
XX
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Sellins KS;
XX
XX WPI: 1999-571822/48.
XX
XX P-PSDB: AAY41079.
XX
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -
XX
XX Claim 1: Page 116-119; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
XX encoding nucleic acid molecules from dogs and cats. The proteins can be
XX expressed by standard recombinant methodology. The nucleic acid molecules
XX and the encoded proteins can be used for preventing or treating diseases,
XX e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
XX development, graft rejection, inflammation, arthritis and atopic diseases
XX such as atopic dermatitis. They can be used in mammals such humans, dogs,
XX cats, cattle, sheep or pets. The products can also be used for detection,
XX diagnosis and drug screening.
XX
XX Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;
XX
XX Query Match 100.0%; Score 996; DB 20; Length 2830;
XX Best Local Similarity 100.0%; Pred. No. 3; 1e-279;
XX Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGCAATTTGTGACAGACTATGGAGTCACTGCTCTGTGATGGCCCTCTG 60
Db 179 AAGGCAATTTGTGACAGACTATGGAGTCACTGCTCTGTGATGGCCCTCTG 238
QY 61 CTCCTGCTGTTCTTCCATGAGAGTCGACGATATTTTCAAGAGAGTGGAGAACTGCCA 120
Db 239 CTCCTGCTGTTCTTCCATGAGAGTCGACGATATTTTCAAGAGAGTGGAGAACTGCCA 298
QY 121 TGGCATTATTAACACCTGCAAAACATTAAGCCTGGATAGCTGTGATATTTTGGCAGAC 180
Db 299 TGGCATTATTAACACCTGCAAAACATTAAGCCTGGATAGCTGTGATATTTTGGCAGAC 358
QY 181 CAGGATAGAGTGTCTGTATGAGATATTCAGAGGCAAGAGAACCTCAAAATGTTTCAT 240
Db 359 CAGGATAGAGTGTCTGTATGAGATATTCAGAGGCAAGAGAACCTCAAAATGTTTCAT 418
QY 241 CTCAAATATTAAGGCGCGTACAGCTTTGACAGAGACAACTGGACCTGAGACTCCACAT 300
Db 419 CTCAAATATTAAGGCGCGTACAGCTTTGACAGAGACAACTGGACCTGAGACTCCACAT 478
QY 301 GTTACAGATCAAGAGGAGGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 360
Db 479 GTTACAGATCAAGAGGAGGACATATCAGTGTTCATCATTAATAAGGGCCCAAGGA 538
QY 361 CTAGTCCCATGACCAAAATGAGTTTCAGACTATCAGTGTTCATCATTAATAAGGGCCCAAGGA 420
Db 539 CTAGTCCCATGACCAAAATGAGTTTCAGACTATCAGTGTTCATCATTAATAAGGGCCCAAGGA 598
```

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins) CC encoding nucleic acid molecules from dogs and cats. The proteins can be CC expressed by standard recombinant methodology. The nucleic acid molecules CC and the encoded proteins can be used for preventing or treating diseases, CC e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor CC development, graft rejection, inflammation, arthritic and atopic diseases CC such as atopic dermatitis. They can be used in mammals such humans, dogs, CC cats, cattle, sheep or pets. The products can also be used for detection, CC diagnosis and drug screening.

Query Match	100.0%	Score 996;	DB 20;	Length 996;
Best Local Similarity	100.0%;	Pred. No. 1,9e-279;		
Matches 996;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGGGCAATTGTGCAGACACATGTGGAGCTAGTACACACTCCCTGGTAGTGGCCCTCTG	60
Db	1	ATGGGCAATTGTGCAGACACATGTGGAGCTAGTACACACTCCCTGGTAGTGGCCCTCTG	60
QY	61	CTCTCTGGTGTCTTCTTCATGAAAGTCAAGCAATATTTTCAACAAGACTGGAGAACTGGCCA	120
Db	61	CTCTCTGGTGTCTTCTTCATGAAAGTCAAGCAATATTTTCAACAAGACTGGAGAACTGGCCA	120
QY	121	TGGCATTTTTAAACCTCTCAAAACATATAAGCTGGATAGCTGGTAGTATTTTGGCAGGAC	180
Db	121	TGGCATTTTTAAACCTCTCAAAACATATAAGCTGGATAGCTGGTAGTATTTTGGCAGGAC	180
QY	181	CAGGATAAGCTGTCTTCTGTATGAGATATTTCAAGAGCAAAAGAAACCTCCAAATGTTCAT	240
Db	181	CAGGATAAGCTGTCTTCTGTATGAGATATTTCAAGAGCAAAAGAAACCTCCAAATGTTCAT	240
QY	241	CTCAAAATATAAGGCGCGCTACAGCGTTTGGACAAAGACAATGGACCGCTGAGACTCCACAT	300
Db	241	CTCAAAATATAAGGCGCGCTACAGCGTTTGGACAAAGACAATGGACCGCTGAGACTCCACAT	300
QY	301	GTTTCAGATCAAGGACCAAGGGGACATATCATCTGTTTCATTATATAAGGGCCCAAGCA	360
Db	301	GTTTCAGATCAAGGACCAAGGGGACATATCATCTGTTTCATTATATAAGGGCCCAAGCA	360
QY	361	CTAGTCTCCCATGCAACCAAAATGAGTCTGACCTATCAAGTGGCTGGTACATTCACATCAACT	420
Db	361	CTAGTCTCCCATGCAACCAAAATGAGTCTGACCTATCAAGTGGCTGGTACATTCACATCAACT	420
QY	421	GAAATTAACAGTAACTTCTTAATAGAACAGAAAATCTTGGCATCAATTAATTTGACCTGCTCA	480
Db	421	GAAATTAACAGTAACTTCTTAATAGAACAGAAAATCTTGGCATCAATTAATTTGACCTGCTCA	480
QY	481	TCTATACAAAGGTTTACCCAGAACTTAAGGAGATGTTATTTTCAAGCTAAACACTGGAAATTCA	540
Db	481	TCTATACAAAGGTTTACCCAGAACTTAAGGAGATGTTATTTTCAAGCTAAACACTGGAAATTCA	540
QY	541	ACTACTAGTATGATTACTGTCTATGATAAATAATCTCAAAATATATGTGACAGAACTGTACAC	600
Db	541	ACTACTAGTATGATTACTGTCTATGATAAATAATCTCAAAATATATGTGACAGAACTGTACAC	600
QY	601	GTTTCTATACACTGGCCCTTTTTCAGTCCCGTGAAGCACACAATGTGAGCGCCTTTTGGCC	660
Db	601	GTTTCTATACACTGGCCCTTTTTCAGTCCCGTGAAGCACACAATGTGAGCGCCTTTTGGCC	660
QY	661	CTGAAACTGGAGACACTGGAGATGCTCTCCCTACCTTTCAATATAGATGACACAACCT	720
Db	661	CTGAAACTGGAGACACTGGAGATGCTCTCCCTACCTTTCAATATAGATGACACAACCT	720
QY	721	AAGGATTAAGACCTGTGAACAAGGCCAATCTCTCTGATTTCCGGCTGTACTTGTAAATGTTT	780
Db	721	AAGGATTAAGACCTGTGAACAAGGCCAATCTCTCTGATTTCCGGCTGTACTTGTAAATGTTT	780

RESULT 2	
AAZ27932/c	
ID	AAZ27932 standard; DNA; 996 BP.

KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; feline;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

PD 23-SEP-1999.

PF 19-MAR-1999; 99WO-US06187.

PR 19-MAR-1998; 98US-0078765.

PR 17-APR-1998; 98US-0062597.

PA (HESK-) HESKA CORP.

PI Sim G, Yang S, Sellins KS;

WP1: 1999-571822/48

New isolated B7 and CTLA4 nucleic acids: used to develop products for

PT treating, e.g., autoimmune and atopic diseases -

PS Claim 1: Page 124-125: 148nn: English
xx

CC The invention provides B7 and CTM4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

SQ Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;

Query Match	100.0%;	Score 996;	DB 20;	Length 996;
Best Local Similarity	100.0%;	Pred. No. 1.9e-279;		
Matches 996; Conservative	0;	Mismatches	0;	Gaps 0

QY 1 ATGGGCAATTGTGACAGCACATATGGGACTGAGTCACACATCTCCTGTGATGGCCCTCCTG 60
|||||
Db 996 ATGGCAATTGTGACAGCACATATGGGACTGAGTCACACATCTCCTGTGATGGCCCTCCTG 937


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Db 480 TGGAAATGAGAGAGAGAGAGCGGCGCTGCAACTTTAATATGTGGAACCAACAATG 421
Qy 874 GAGAGAAAAGAGAGCAAGACAGCAACGAGTACCATCCAGTACCTGAGATCT 933
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 420 GAGAGGAAGAGAGTGAAGAGAGCAAGAAAAGAAAATTCATATACCTGAAAGATCT 361
Qy 934 GATGAAGCCAGTGT--TATTACATTTTGAAGACAGCCTCAGGGCAGCAAAAGTACTACA 990
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 GATGAACCCAGCTGTGTTTAAAGTTGGAAGACATCTTCATGCGACAAAAGTATACA 301
Qy 991 CATTTT 996
    |||||
Db 300 TCTTTT 295

RESULT 13
Bg001664 347 bp mRNA linear EST 24-JAN-2001
LOCUS RC4-GN0067-151100-016-b07 GN0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg001664
VERSION Bg001664.1 GI:12440219
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
    Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
    Nagai, M.A., da Silva, W. Jr., Zaago, M.A., Bordalo, S., Costa, F.F.,
    Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
    Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
    M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
    Simpson, A.J.
    Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202653
COMMENT Contact: Simpson A.J.G.
    Laboratory of Cancer Genetics
    Ludwig Institute for Cancer Research
    Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
    Brazil
    Tel: +55-11-2704922
    Fax: +55-11-2707001
    Email: asimpson@ludwig.org.br
    This sequence was derived from the FAPESP/LICR Human Cancer Genome
    Project. This entry can be seen in the following URL
    (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-GN0067-
    151100-016-b07&t3=2000-11-15&t4=1)
    Seq primer: puc 18 forward
    High quality sequence start: 19
    High quality sequence stop: 347.
    Location/Qualifiers
        1..347
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="GN0067"
        /dev_stage="Adult"
        /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
        ; Site_2: SmaI; A mini-library was made by cloning
        products derived from ORSPRS PCR (U.S. Letters Patent
        application No. 196,716 - Ludwig Institute for Cancer
        Research) profiles into the puc 18 vector. Reverse
        transcription of tissue mRNA and cDNA amplification were
        performed under low stringency conditions."
BASE COUNT 109 a 75 c 75 g 88 t
ORIGIN
Query Match 11.0%; Score 109.8; DB 10; Length 347;
Best Local Similarity 62.6%; Pred. No. 1.4e-16;
Matches 171; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
Qy 679 GAGATGCTGCTCTCCCTACCTTTCAATATATAGTGCACACACTAAGTAAGACCCCTGAA 738

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Db 50 GACAAGACGGGGCTTTTATCTTTCACCTTTCTCCTACAGAGTTGAGAGCCCTCAGCTCCC 109
Qy 739 CAAGCCACATCTCTCTGATTCGGCGCTGTACTGTATGTTGTTGTTTGTGGATG 798
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 CCAGACCACATCTCTCTGATTCAGCTGTACTTCCACACTTATATATGATGATGTT 169
Qy 799 GTCTCTTTTAAACACTAAGAAAAGAGAGAGCAGCGCCCTCATGTAATG 858
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 TTCTGTCTAATCTATGGAATGGAAGAGAGAGAGCGCTCGCAACTTTTAAATGT 229
Qy 859 GAAACCATCAAAAGAGAGAGAGAGAGCAACAGACCAAGAGATACCATCAC 918
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 GGAACCAACAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
Qy 919 GTACCTGAGATCTGTGATGAAGCCCACTAT 951
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 ATACCTGAAGATCTGATGAAGCCCACTGTT 322

RESULT 14
A1093604 570 bp mRNA linear EST 10-NOV-1998
LOCUS C082B09.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1634297 3' similar to SW:CD86_HUMAN P42081 r LYMPHOCTYE
ACTIVATION ANTIGEN CD86 PRECURSOR ;, mRNA sequence.
ACCESSION A1093604
VERSION A1093604.1 GI:3432580
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
    1 (bases 1 to 570)
    NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
    National Cancer Institute, Cancer Genome Anatomy Project (CCAP),
    Tumor Gene Index
    Unpublished (1997)
    Contact: Robert Strausberg, Ph.D.
    Email: cgrabs-r@mail.nih.gov
    This clone is available royalty-free through LNL; contact the
    IMAGE Consortium (info@image.lnl.gov) for further information.
    Insert length: 801 Std Error: 0.00
    Seq primer: -40m13 fwd. ET from Amersham
    High quality sequence stop: 400.
    Location/Qualifiers
        1..570
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="IMAGE:1634297"
        /clone_1lb="Soares_NSF_F8_9W_OT_PA_P_S1"
        /lab_host="DH10B"
        /note="Organ: pooled; Vector: pT7TD-pac (Pharmacia) with
        a modified polylinker; Site_1: Not I; Site_2: Eco RI;
        Equal amounts of plasmid DNA from five normalized
        libraries were mixed, and ss circles were made in vitro.
        Following HAP purification, this DNA was used as tracer in
        a subtractive hybridization reaction. The driver was
        PCR-amplified cDNAs from pools of 5,000 clones made from
        the same 5 libraries. The pools consisted of the following
        libraries and clones: Soares NBHSF pool 1:
        309384-310919, 323208-325895 Soares NB2HP pool 1:
        145032-147335, 147720-148103, 148872-149255, 15002 -
        150407, 151176-152327 Soares NB2HF8-9W pool 1:
        758280-760583, 772104-774407 Soares NBHPA pool 1:
        304776-306311, 320136-322823, 326280-326663 Soares NBHOT
        pool 1: 723720-726407, 739080-740999 Subtraction by Bento
        Soares and M. Fatima Bonaldo."
BASE COUNT 150 a 107 c 134 g 179 t
ORIGIN
Query Match 10.5%; Score 105; DB 9; Length 570;
Best Local Similarity 66.9%; Pred. No. 2.2e-15;

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Db	635	ACAGACATTACAGAACTGT	654
RESULT 9			
LOCUS	AM427922	257 bp	linear
DEFINITION	64549 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.		EST 25-APR-2001
ACCESSION	AM427922		
VERSION	AM427922.1	GI:6955869	
KEYWORDS	EST.		
SOURCE			
ORGANISM	Bos taurus		
COW	Eumariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
REFERENCE			
AUTHORS	Smith,T.P.L., Grosse,W.M., Fekling,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G., Pertes,G., Holt,L., Karanycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.		
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle		
JOURNAL	Genome Res. 11 (4), 626-630 (2001)		
MEDLINE	21180013		
COMMENT	Contact: Smith TPL PO Box 166, Clay Center, NE 68935-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smitht@mail.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 20 and -minmatch 12 options. PCR primers FORWARD: AGGAACACGCTATGACCAT BACKWARD: GTTTCACGTCACGACG Plate: 30 row: G column: 20 Seq primer: ATTGAGGACACTATG. Location/Qualifiers 1..257 /organism="Bos taurus" /db_xref="taxon:9913" /clone_id="MARC 3BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI; library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal Longissimus muscle."		
FEATURES			
SOURCE			
BASE COUNT	80 a 64 c 52 g 61 t		
ORIGIN			
Query Match	18.0%;	Score 179.2;	DB 9;
Best Local Similarity	81.2%;	Pred. No. 1.1e-33;	Length 257;
Matches 208;	Conservative 0;	Mismatches 48;	Indels 0;
		Gaps 0;	
115	CTCGCATGCCATTTTACAACTCCAAACAAACATTAAGCCGTGATGAGCTGATATTTGG	174	
Db	2 CTGCGCATGCCATTTTCCAAACACCCAAACCTCGAGCCGTGATGATATTTGG	61	
QY	175 CAGGACCAAGATTAAGCTGTGTTCTATGACATATTTCAGAGCAAGAGAACCTTCAAT	234	
Db	62 CAGATTCAGATTAAGTGTGTTCTCTATGAGCTATTTCAGAGCAAGAGAACCCCAAT	121	
QY	235 GTTATCTCAATATTAAGGCGCTTACAGAGCTTTACAAAGCAACAGACCTGAGACT	294	
Db	122 GTTAATCCCAAGTATTAAGGCGCCACCAAGCTTGACCAAGAGACAGTGGACCTGAGACT	181	
QY	295 CACAATGTGACAGCAAGAGCAACAGATATGACGTGTTTCATTCATTAATAAGGCCC	354	
Db	182 CACAAGCTTCAATCAAGACACAGGCTCGATTAAGTGTTCATTCATTAAGAGAGTCC	241	

OY	355	AAGAAGCTAGTCCCA	370
DB	242	CAGAAGTTGGTTCCA	257
RESULT_10			
AW516826			
LOCUS	x94oh01.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone IMAGE:2748913 / similar to SW:CD86_HUMAN P42081 T LYMPHOCTE ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.	496 bp	EST 03-MAR-2000
ACCESSION	AW516826		
VERSION	AW516826.1	GI:7154992	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	I (bases 1 to 496)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-i@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40UP from GIBCO High quality sequence: slbp: 458. Location/Qualifiers 1..496 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2748913" /clone_lib="Soares_NHCEC_cervical_tumor" /tissue_type="tumor" /lab_host="DH10B (phage-resistant)" /note="Organ: cervix; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5' TGATACCATTGTGAAGTCGAGCGGCCGCAGAGTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized; constructed by Bento Soares and M.Patlna Bonaldo."		
FEATURES			
SOURCE			
BASE COUNT	156 a	102 c	93 g 145 t
ORIGIN			
Query Match	12.5%	Score 124.2;	DB 9; Length 496;
Best Local Similarity	63.9%;	Pred. NO. 4.le-20;	
Matches 203; Conservative	0; Mismatches 113;	Indels 3; Gaps 1;	
OY	679	GAGATGCTGCTCTCCCTACCTTTCAATATAATAGATCACAAACTAAGAGATTAAGACCTTGAA	738
Db	59	GACAAGAGCGGGCTTTATATCTTACCTTTCTCTATAGAGCTTAGAGACCCCTACACCTCCC	118
OY	739	CAGAAGCATCTTCTCTGAGTTGGCGCTGTACTGTAATGTTGTTGTTTTTTGTGGGATG	798
Db	119	CCAGACCACATCTCTTGGATTACAGCTGTACTTCCACAGTTATATATGTGTGNTGGT	178
OY	799	GTCGCTTTAANAACATAAGAAAAGAAAGAAAGAACGAGCGCTGCCCTCTCATGAAATG	858
Db	179	TTCTGTCTAATTCTATATGGAATGGAAGAGAGAGGGCTCGCAAATCTTATAATGT	238
OY	859	GAACCATCAAAAGGAGAGAAAAAGAGAGCAACAGACCAACGAAAGAGTACATACCAC	918
Db	239	GGAACCAACACATATGAGAGGAGAGAGTGAACAGACCAAGAAAAGAAAAAATCAT	298
OY	919	GTACTCTAGAGATCTGATGAAGCCAGT---TATTACATTTTGAAGACAGCCTCAGGC	975
Db	299	ATACCTGAAMGATCTGTATGAAGCCACAGTGTATTTTAAAGTTTGAAGACATCTTATTCG	358

OY	613	TTGCCCTTTTTCAGTCCCTGAGACACACATGTGAGCGCTCTTTTGTGCCCTGAACTGAG	672
Db	393	GTGTCCTTCCATCCATCCCTCCGAGACAATGTGACACATNCTGTGCTCCGACACTTGAG	334
OY	673	ACATCGAGAGA---TCTGCTGTCCTTACCTTTCAATATAGATGCAACCACTTAAGATATA	729
Db	333	CCACACAGACACACGCTTTTCTCCTTACCTTGTATATAGATGCCAAGCCACCTGTGCA	274
OY	730	GACCCGTGAACAAGGCCACTTCCCTGTGATTCGCGCTGACTTGTATATTTTGTGTTT	789
Db	273	CCCCCTGCCACAGACACATCCTTNGATGATGAGCTTACTTGTATACAGTGTGTTGTG	214
OY	790	TGTGGGATGATGCTCTTATAAAGCTTAAGAAAGAAAGAAAGAACACCTTGCCCTCT	849
Db	213	TGTGGGATGATGCTCTTGTATAACACTTAAGAAAGAAAGAAAGAACACCTTGCCCTCT	154
OY	850	CATGAT---TGAAACCATCAAAAGGAGAGAAAGAGACAAACACACCAAGCAAGA	906
Db	153	AATGATATGTGTGAACCATCAAAATGAAACAGAGAGGCGATGAACCAACTATAGACAG	95
OY	907	GTACCATACACGTAACCTGAGAGATCTGATGAGGCCAGTG--TATTACATTTTGAAG	963
Db	94	-----AAGTCCATGAACGATCTGATGATGCCAGTGATGATGTTAATATTTTNAAG	45
OY	964	ACAGCCTCAGGCGCAAAAGTACTACATATTTT	996
Db	44	ACAGCCTCAGATGACACACGTAACATTTT	12
RESULT 8			
LOCUS	BB635605	654 bp mRNA	linear EST 26-OCT-2001
DEFINITION	BB635605 RIKEN full-length enriched, 0 day neonate thymus Mus		
ACCESSION	BB635605		
VERSION	BB635605.1	GI:16471650	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 654)		
	Arakawa,T., Carinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,T., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takehashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-8222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp/ URL: http://genome-gsc.riken.go.jp/ Carnici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) waghi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1751-1771 (2000)		

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakita, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.,
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.
Location/Qualifiers
1..654
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A430076L06"
/clone_id="RIKEN full-length enriched, 0 day neonate thymus"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site:1; Site:2; BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAAGATCCACAGACGCTCTTTTGTTCCTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCGAGTAATAATTATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from LambdaFLC I."

	BASE COUNT	148 a	151 c	152 g	202 t	1 others
ORIGIN						
Query Match	20.2%; Score 201.4; DB 9; Length 654;					
Best Local Similarity	70.5%; Pred. No. 4.le-39;					
Matches 268; Conservative	0; Mismatches 112; Indels 0; Gaps 0;					
QY	15 CAGCACTATGGAGACTGAGTCACTCTCTCTGTATGGCCCTCGCTCTGTGGTTTC	74				
Db	275 CTGCACCATGAGCGCTTGCGCAATCTTATCTTGTGACAGCTCTTGCGATGTCAGATCGT	334				
QY	75 TTTCATGAAGAGTCAAGATATTTCAACAAGACTGGAAGACTGCCATCCATTTTACAA	134				
Ddb	335 TTCCGTGGAGAGCGCAAGCTTATTTCAATGGAGCTSCATATCTGCCGTCCCATTTACAA	394				
QY	135 CTCCTAAAAACATTAAGCTTGATGAGCTGTAGTATTTTGGCAGACCGAGTAAGCTGGT	194				
Dd	395 GGCTAAAACATTAACCCTGAGTACCTGTAGTATTTTGGCAGGACCGACAAAGTTGGT	454				
QY	195 TCTGTATGAGATATTTACAGGCGCAAGAGAACCCCTAAATGTCTTCATCATATTAAGG	254				
Dd	455 TCTGTACGACGACCTATTGGGCGCACAGAAACTTGATATGTGTGAATGCCAAGTACTGNG	514				
QY	255 CGGTACAAGCTTTGACAAGACACTGGACCCCTGAGACTCCACAATGTTTCAGATCAAGA	314				
Dd	515 CCGCAGCGAGCTTTGACAGAGAACCAACTGACCTACGACTTCACATGTTTCAGATCAAGA	574				
QY	315 CAAGGCGCATATACCTCTTTCATTCATTNTAAAGGGCCCAAGAGCTAGTCCCATGCA	374				
Dd	575 CATGGGCTCGTAGTGTGTTTATTATCAAAAAAAGCCACCCACAGAGATCAATTAATCTCC	634				
QY	375 CCNAATGAGTCTCGACTAT	394				

QY 622 TCAGTCCCTGAAG 634
 DB 684 TCATCCCGGATG 696
 RESULT 6
 LOCUS BM089797 578 bp mRNA linear EST 19-NOV-2001
 DEFINITION 503647 MARC 2Bov Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BM089797
 VERSION BM089797.1 GI:17000425
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 578)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G.,
 Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keefe,J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 CONTACT: Smith RPL
 USDA, ARS US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402/762 4366
 Fax: 402/762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.
 PCR PRIMERS
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCAGCAG
 Plate: 5 row: D column: 18
 Seq primer: ATTGTAGTACCTATGAC.
 FEATURES
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 /db_xref="taxon:9913"
 /clone_lib="MARC 2BOY"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 library made from pooled tissue from testis, thymus,
 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."
 BASE COUNT 170 a 150 c 120 g 137 t 1 others
 ORIGIN
 Query Match 26.1%; Score 259.6; DB 10; Length 578;
 Best Local Similarity 76.9%; Pred. No. 1.9e-53;
 Matches 339; Conservative 0; Mismatches 80; Indels 22; Gaps 1;
 QY 17 GCACATATGGGACGTGACCTCTCTGATGAGCCCTCTGCTCTGCTGTTCTT 76
 DB 137 GCACCATGGGACCTGCAAACTCTATATGATGAGCCCTCTGCTCTGTTCCACG 196
 QY 77 -----CCATGAGAGTCAACATATTTCAACAGACTGGAGAA 114
 DB 197 TTCCTTTTCAGTGTGCTCTCTTNGAAAATCATGCTTTCTTAAGAGACTGAGAA 256
 QY 115 CTGCATGCAATTTTCAAACTCAAAACATTAAGCTGGATGACCTGTATATTTGG 174
 DB 257 CTGCATGCACTTTCACAAACCAAACTCAAGCTGAGAGACTGTGTATATTTGG 316
 QY 175 CAGGACGAGATTAAGCTGTCTGTATGAGATATTCAGAGGCAAGAGAACCTCAAAAT 234

DB 317 CAGATCAGAAATAAGTTGGTCTCTATGAGCTATTCAAGGCCAAGAGCAAGCCAAATAT 376
 QY 235 GTTCATCTCAATATTAAGGGCGGTACAGACTTTGACAGCACTGACCTGAGACT 294
 DB 377 GTTAATCCCAAGTATATAGCGCCGACAGACTTTTACAGGACACTTGGACCTTGAGCTC 436
 QY 295 CACAATGTTCAAGATCAAGGACCAAGGACACATATCACTGTTTCATTATTAAGGGCCC 354
 DB 437 CACAACGTTCAATCAAAAGACACAGGCTGATCAAGTTTCATTCACATAGAAAGCTCC 496
 QY 355 AAAGACTAGTTCCTCCATGACCAACCAATGAGTTCTACCTATCACTGCTTGAATTAGT 414
 DB 497 CAGAGATGTGTTTCATCCACACAGATGAGTTCTGACCTGATAGTGTGGCTAACTTCACT 556
 QY 415 CAACCTGAATTAACGTAAC 435
 DB 557 CAACGAGAAATTAAGCTAATT 577
 RESULT 7
 LOCUS AA056905/c 512 bp mRNA linear EST 18-SEP-1996
 DEFINITION ES1224F Pig Spleen lambda gt 11 Library (Clontech Cat # PL1006b)
 SUS scrofa cDNA clone SPL224 forward similar to L25259 CTUA4
 counter-receptor , human, mRNA sequence.
 ACCESSION AA056905
 VERSION AA056905
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 512)
 Tugule,C.K., Wahls,S. and Schmitz,C.
 TITL Epressed Sequence Tags from pig Spleen
 JOURNAL Unpublished (1996)
 COMMENT
 Contact: Tugule CK
 Molecular Genetics Laboratory, Department of Animal Science
 Iowa State University
 201 Kildee Hall, Ames, IA 50011-3150, USA
 Tel: 5152944252
 Fax: 5152942401
 Email: ctugule@iastate.edu
 PCR PRIMERS
 FORWARD: TGGCGAGACTCCTG
 BACKWARD: GACCGCGCTCAGCT
 Insert Length: 950 Std Error: 50.00
 Seq primer: TGGCGAGACTCCTG.
 FEATURES
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 1..512
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 /db_xref="taxon:9823"
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 /clone_lib="Pig Spleen lambda gt 11 Library (Clontech cat
 # PL1006b)"
 /tissue_type="spleen"
 /dev_stage="adult"
 /note="Oligo (dtr) primed"
 BASE COUNT 125 a 106 c 114 g 163 t 4 others
 ORIGIN
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 Best Local Similarity 74.3%; Pred. No. 4.7e-50;
 Matches 381; Conservative 0; Mismatches 111; Indels 21; Gaps 5;
 QY 493 TACCAGAACTAAGAGATATATTTACGCTAAACACTGAGATTAACACTAGATAT 552
 DB 512 TACCAGAAACCCAGAGATGATATATGTTGCTAATATCGAAGATTTACACACTGACAT 453
 QY 553 GATCTGATGAAGAATATCAAAATATAGTGCACAGACTGTATCAAGCTTTCTATCAGC 612
 DB 452 GATGCTGACATGAAGAATATCAAAATATACATCAC-GGANTTTACATGTATATCAGG 394

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 027. Note: this is a NIH-MGC Library."

BASE COUNT

227 a 166 c 156 g 204 t

Query Match 40.1%; Score 399.2; DB 10; Length 753;
Best Local Similarity 82.3%; Pred. No. 8.4e-88;
Matches 507; Conservative 0; Mismatches 103; Indels 6; Gaps 4;

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QY 17 GCACATGAGGAGTGCACACTCTCTGTATGGCCCTCCTGCTCTGTGTTCTT 76
    |||
Db 120 GCACATGAGGAGTGCACACTCTCTGTATGGCCCTCCTGCTCTGTGTTCTT 179
QY 77 CCATGAGAGTGCACACTCTCTGTATGGCCCTCCTGCTCTGTGTTCTT 136
    |||
Db 180 CTTCTGAAGTGCACACTCTCTGTATGGCCCTCCTGCTCTGTGTTCTT 239
QY 137 CTCGAATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 196
    |||
Db 240 CTCGAATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 299
QY 197 TGTATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 255
    |||
Db 300 TGTATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 359
QY 256 CGTACAGGCTTGCACAGGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 315
    |||
Db 360 CCGACAGGCTTGCACAGGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 419
QY 316 AAGGCGACATGACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 375
    |||
Db 420 AAGGCGCTGTATGACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 479
QY 376 CAATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 435
    |||
Db 480 CAGATGATGACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 539
QY 436 TCTATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 495
    |||
Db 540 TCTATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 596
QY 496 CAGAAAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 555
    |||
Db 597 CAGAAAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 655
QY 556 ACT-GTCATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 614
    |||
Db 656 GGTATGAGTGCACACTCTGTATGGCCCTCCTGCTCTGTGTTCTT 715
QY 615 GCCTTTTTCAGTCCCT 630
    |||
Db 716 GTCTGTTTCATTCCTT 731
```

RESULT 2
B1824940 655 bp mRNA linear EST 04-OCT-2001
LOCUS B1824940
DEFINITION 60303254F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173789 5',
RNA sequence.
ACCESSION B1824940
VERSION B1824940.1 GI:15936490
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 655)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LIML1432 row: 1 column: 14
High quality sequence start: 27
High quality sequence stop: 653.
Location/Qualifiers

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male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research genetics tracking code
021. Note: this is a NIH-MGC Library."
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BASE COUNT 194 a 147 c 145 g 169 t

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Matches 411; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

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RESULT 3

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 1187.05 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-28

Perfect score: 996
Sequence: 1 atggcatttgtagacagcac.....acaaagtactacacattt 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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BI906246
ACCESSION
BI906246
VERSION
BI906246.1 GI:16168907
KEYWORDS
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human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 753)
NIH-MGC http://mgc.ncl.nih.gov/
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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cloning). Average insert size 1.7 kb, insert size range

FEATURES

source

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ACCESSION L25259
VERSION L25259.1 GI:416368
KEYWORDS CTLA4 counter-receptor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1112)
Freeman,G.U., Gribben,J.G., Boussioutis,V.A., Ng,J.W., Restlivo,V.A.,
Jr., Lombard,D.A., Gray,G.S., and Nadler,L.M.
Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human
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Science 262 (5135), 909-911 (1993)
94053735

JOURNAL
MEDLINE
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DEFINITION Sequence 33 from patent US 6251627.
ACCESSION AR159758
VERSION AR159758.1 GI:16222530
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Cai, Z., Sprent, J., Brunmark, A., Jackson, M. and Peterson, P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6251627-A 33 26-JUN-2001;
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Query Match 54.2%; Score 540; DB 6; Length 1002;
Best Local Similarity 75.4%; Pred. No. 4e-136;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;
QY 17 GCACATATGGAGCTGAGTACACTCTCTGTGATGGCCCTCTGCTCTGTGTTCTT 76
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LOCUS AR160450
DEFINITION Sequence 33 from patent US 6255073.
ACCESSION AR160450
VERSION AR160450.1 GI:16224366
KEYWORDS
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 1002)
AUTHORS Cai, Z., Sprent, J., Brunmark, A., Jackson, M. and Peterson, P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6255073-A 33 03-JUL-2001;
FEATURES
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BASE COUNT 309 a 215 c 203 g 275 t
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Query Match 54.2%; Score 540; DB 6; Length 1002;
Best Local Similarity 75.4%; Pred. No. 4e-136;
Matches 743; Conservative 0; Mismatches 225; Indels 18; Gaps 5;
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Db	879	GAGGACCTCAGGCTCCGCCACAGCACATCTCTTGATATACAGCTGTACTTCCACAGTT	938
OY	781	GTTGTTTTTGTGGAGATGTTGTCCTTTAAACACTAAGGAAAGGAGAGACAGACGCT	840
Db	939	ATTAATATGTGTGATGGTTCCTGCTCTAATCTTATGGAATGTGAAGAAAGAGGGCT	998
OY	841	GGCCCTCTCATGATGTGAACAACATCAAAAGGGAGAGAAAGAGACCAACAGCCACAC	900
Db	999	CGCAACTCTTTTAAATGTGGAAACCAACCAATGTGAGAGGAGAGATGAACAGACACAG	1038
OY	901	GAAGAGTACCATACCACTGACTGAGAGATCTGATGTAAGCCCACTG--TATTAACATT	957
Db	1059	AAAAGAGAAAATTCATATACCTGAAAGATCTGATGTAAGCCCACTGTTTAAAGT	1118
OY	958	TTGAAGACAGCCTCAGGCGACAAAAGTCTACACATTTT	996
Db	1119	TGGAAGACATCTCTATGCGACAAAAGATACATGTTTT	1157
RESULT 12			
LOCUS	ARI47736	1002 bp	DNA
DEFINITION	Sequence 33 from patent US 6225042.	linear	PAT 08-AUG-2001
ACCESSION	ARI47736		
VERSION	ARI47736.1	GI:15111826	
KEYWORDS			
SOURCE	unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1002)		
AUTHORS	Cal, Z., Sprent, J., Brunmark, A., Jackson, M. and Peterson, P. A.		
TITLE	Antigen presenting system and methods for activation of T-cells		
JOURNAL	Patent: US 6225042-A 33 01-May-2001;		
FEATURES	Location/Qualifiers		
SOURCE	1..1002		
BASE COUNT	309 a	215 c	203 g
ORIGIN			275 t

QY	17	GCACATGAGGACGTGACGTACACATCTCCTTGATATGGGCCCTCCGCTCGCTGGTGTTCCT	76
Db	20	GCACATGAGGACGTGAGTACACATCTCTTGTGTGATGGCCCTTCGCTCTCTGGTGTCTGCTC	79
QY	77	CCATGAGAGTCAAGCAATATTTCAACAGACTGGAACTGGCATGCCATTTTACAAACT	136
Db	80	CTCGAAGATTCAAGCTTATTTCAATGAGACTGCACACCTGGCATGCCAATTTGGCAACT	139
QY	137	CTCAAAACATATAGCCTGGATGAGTGGTACTATTTTGGAGAGCAGAGATTAAGCTGGTTC	196
Db	140	CTCAAAACCAAGCCTGATGAGTGAAGTATATTTTGGCAGGACAGGAAACTTGGTTC	199
QY	197	TGTATGAGATATTCAGAGGCAAGAGAAACCCCAAAATGTTCATCTCAATTAAGGGCC	256
Db	200	TGAATGAGGTATCTATGAGCAAGAGAAATTTGACAGTGTCTATTCAGATATATGGGCC	259
QY	257	GTACAGGCTTTGACAGAGACACTGGGACCCCTGGAGACTCCCATTTGTCAGATCAAGGACA	316
Db	260	GTACAGGTTTGGATTCGGACACTTGGACCTGGAGACTTCACAACTTTCAGATCAAGGACA	319
QY	317	AGGGCACTATCTACTGTTTCAATTCATTATAAAGGGCCCCAAGSAGTATGTTCCCATGCAC	376
Db	320	AGGGCTTATCAATGTTATCATTCATCCATCACAAAAAGCCACAGGAATGATTCGATCCACC	379
QY	377	AATATAGTTCGACCTATACAGTGGTCTCTAATCACTCAACTGGAATATACAGTACTT	436
Db	380	AGATCAATTCGAACTGTCACTGCTTGTCTAATCTTCACTCACTGAAATATGATCAATTT	439
QY	437	CTAATATGAAGAAAAATTTCTGGCATCTATAAATTTGACCTGCTCATCTATACAAAGTTTACC	496
Db	440	CTAATATTAACAGAAAA--TGTGTACATTAATTTGACCTGCTCATCTAATACAGGGTTACC	496
QY	497	CAGAACCTAAGAGATGTTATTTTCAAGTAAACATGTGAATTCACACTACATATATGATA	556
Db	497	CAGAACCTTAAGAGATGAGTGTGTTTGTCTAAGACCAAGAATTTAATCATCGATATGATGAG	556
QY	557	CTGTGATGAGAAATCTCAAAATATATGTGACAGAACTGTACAAAGTTTATCAGCTTCC	616
Db	557	GTATATATGAGAAATCTCAAGATATATGTACAGAACTGTACAGAACTTTCATCAGCTTGT	616
QY	617	CTTTTTCAGTCCCTGAAG---CACACAATGAGACCGTCTTTTGGCCCTGAACCTGAGAG	673
Db	617	CTGTTTCATTTCCCTATGTATTACGAGCAATATACCATTTCTGTATTTCTGGAACCTGACA	676
QY	674	CACGTAGATGTGCTCTCCCTACCTTCAATATATGATGCAACAACCTTAAGATTAAGAAC	733
Db	677	---AGAGCGGGCTTTATCTTCACCTTCTCTATAG-----ACCTTGAGAGACCTCAGC	727
QY	734	CTGACACAGGCCACTCTCTCGATGTGGGCTGTGATCTGTAATGTGTGTTTGTGTTG	793
Db	728	CTTCCCCCAACACACTCTCTTGGATTTACAGCTGTATCTCCACAGTATATATATGTGTGA	787
QY	794	GGATGTGTCTCTTTAAACACTAAGGAAAAGGAAGAAAGACAGCCCTGGCCCTCATG	853
Db	788	TGTTTTTCTCTAATCTCATGAAATATGAGAAAGAAAGAGAGCGGCTCCGCAACTTTATA	847
QY	854	AATGTGAACCATCAAAAGGGAGAGAAAAGAGACAAACAGCAACGAAGAGTACCAT	913
Db	848	AATGTGAACCAACCAAAAGGAGAGAGAGAGAGAAACACCAACAAAGAGAGAAAAA	907
QY	914	ACCACCTACTCAGAGATCTGATGAGAGCCCAAGT---TATTACATTTTGAAGACAGCT	970
Db	908	TCCATTTACTCTGAAGATCTGATGAGAGCCCAAGCGTGTTTTAAAGTTCGAAGACATCTT	967
QY	971	CAGGCGACAAAGTACTACACATTTT	996
Db	968	CATGCGACAAAGTATATCATGTTT	993

Query Match	54.2%;	Score 540;	DB 6;	Length 1002;
Best Local Similarity	75.4%;	Pred. No. 4e-136;		
Matches 743;	Conservative	0;	Mismatches 225;	Indels 18;
				Gaps 5;

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TRLSPFSILEDPOPPDHIPWITAVLPVITCVMPFCILIMKKKKRPRNSYK
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BASE COUNT 429 a 306 c 284 g 405 t
ORIGIN

Query Match 55.5%; Score 553; DB 9; Length 1424;
Best Local Similarity 75.7%; Pred. No. 1.1e-139;
Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;
OY 4 GGCATTGTGACGACATATGGGACATGCTCCTCTTGATGAGCCCTCCTGCTC 63
DB 130 GGCATTGTGACGACATATGGGACATGCTCCTCTTGATGAGCCCTCCTGCTC 189
OY 64 TCTGCTGTTCTTCATGAGATGATGATGATGATGATGATGATGATGATGATG 123
DB 190 TCTGCTGCTGCTCCTGATGATGATGATGATGATGATGATGATGATGATGATG 249
OY 124 CATTTTCAAACTCTCAAAACATATAGCCTGATGATGATGATGATGATGATGATG 183
DB 250 CAATTTGCAAACTCTCAAAACATATAGCCTGATGATGATGATGATGATGATGATG 309
OY 184 GATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
DB 310 GAAATATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 369
OY 244 AAATATAGGGGCTTACAGCTTTGACAGGACAACTGACCCCTGAGACTCCAAATGTT 303
DB 370 AAGTATATGGGCGCACAGTTTGTGACAGTTGACCCCTGAGACTCCAAATGTT 429
OY 304 CAGATCAAGGACGACGACATATGATGATGATGATGATGATGATGATGATGATG 363
DB 430 CAGATCAAGGACGACGACATATGATGATGATGATGATGATGATGATGATGATG 489
OY 364 GTTCCATGACGACGACGACATATGATGATGATGATGATGATGATGATGATGATG 423
DB 490 ATTGCATCCACGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 549
OY 424 ATACAGATTAATCTTAATAGACGAAATTTGGCATTAATTTGACCTGCTCATCT 483
DB 550 ATAGTACCAATTTCTAATATACGAAAA--TGTGTACATTAATTTGACCTGCTCATCT 606
OY 484 ATACAGGTTACCCAGAACTTAAGGAGATGATTTTCACTTAACCTGAGATTTCAACT 543
DB 607 ATACAGGTTACCCAGAACTTAAGGAGATGATTTTGTGTAAGAACCAAGATTTCAACT 666
OY 544 ACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 603
DB 667 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
OY 604 TCTATAGCTTGGCTTTTTCAGTCCCTGAAG---CACACATGTTGAGCTCTTTTGTGCC 660
DB 727 TCCATAGCTTGGCTTTTTCAGTCCCTGAAG---CACACATGTTGAGCTCTTTTGTGCC 786

OY 661 CTGAAGCTGGAGACATGAGATGCTGCTGCTTACCTTTCATATAGATGCACAACT 720
DB 787 CTGGAAGCTGCA---AGACCGGCTTTTATCTTACCTTCTCTAAG-----AGCTT 837
OY 721 AAGGATTAAGACCTCTGAACAAGGACCACTTCTGATGATGATGATGATGATGATG 780
DB 838 GAGACACCTCAGCCTCCGCCAGACACATCTCTTGATTTACACTGTACTTCCACAGTT 897
OY 781 GTTGTCTTTTGTGGATGTTGCTCTTTAAACACTAAGAAAGAAAGAAAGACGCT 840
DB 898 ATTATATGTGTGATGCTTTTCTGCTAATCTATGAAATGAAAGAAAGAAAGACGCT 957
OY 841 GGCCCCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 958 CGCACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1017
OY 901 GAAAGATACCATACGACGATGATGATGATGATGATGATGATGATGATGATGATG 957
DB 1018 AAGAGACCAAAATCCATATACCTGATGATGATGATGATGATGATGATGATGATG 1077
OY 958 TTGAGACACGCTCAGGCGCAAAAGTACTACATTTT 996
DB 1078 TCGAAGACATCTTCATGCGACAAAGATGATGATGATTTT 1116

RESULT 11
AX188198
LOCUS AX188198
DEFINITION Sequence 3893 from Patent WO0142467.
ACCESSION AX188198
VERSION AX188198.1 GI:15139671
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2205)
AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.
TITLE Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
JOURNAL Patent: WO 0142467-A 3893 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
FEATURES
source location/Qualifiers
1..2205
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 650 a 477 c 466 g 610 t 2 others
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Query Match 55.5%; Score 553; DB 6; Length 2205;
Best Local Similarity 75.7%; Pred. No. 1.1e-139;
Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;
OY 4 GGCATTGTGACAGACATATGGGACATGCTCCTCTTGATGAGCCCTCCTGCTC 63
DB 171 GGCATTGTGACAGACATATGGGACATGCTCCTCTTGATGAGCCCTCCTGCTC 230
OY 64 TCTGCTGTTCTTCATGAGATGATGATGATGATGATGATGATGATGATGATGATG 123
DB 231 TCTGCTGCTGCTCCTGATGATGATGATGATGATGATGATGATGATGATGATG 290
OY 124 CATTTTCAAACTCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATGATG 183
DB 291 CAATTTGCAAACTCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATG 350
OY 184 GATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
DB 351 GAAACCTTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 410
OY 244 AAATATAGGGGCTTACAGCTTTGACAGCAAGCAACTGAGCCCTGAGACTCCAAATGTT 303
DB 411 AAGTATATAGGGGCGCACAGTTTTCATGCGACAGTTTGGACCTGAGACTTCCAAATCTT 470

QY 958 TTGAAGACAGCCTCAGCGACAAAAGTACTACATTTT 996
 Db 1078 TCGAAGACATCTTCATCGCACAAAAGTACTACATGTTTT 1116

RESULT 9
 AX332506 1424 bp DNA linear PAT 09-JAN-2002
 LOCUS Sequence 3015 from Patent WO0194629.
 DEFINITION AX332506
 ACCESSION AX332506
 VERSION AX332506.1 GI:18123140
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (sites)
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
 gene sets
 Patent: WO 0194629-A 3015 13-DEC-2001.

TITLE
 gene sets

JOURNAL
 Avalon Pharmaceuticals (US)

FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 429 a 306 c 284 g 405 t

ORIGIN

Query Match 55.5%; Score 553; DB 6; Length 1424;
 Best Local Similarly 75.7%; Pred. No. 1..1e-139;
 Matches 756; Conservative 0; Mismatches 225; Indels 18; Gaps 5;

QY 4 GGCATTTGTGACAGCAGTATGAGTACAGTCTCTCTTGATGGCCCTCTGTC 63
 Db 130 GGCATTTGTGACAGCAGTATGAGTACAGTCTCTCTTGATGGCCCTCTGTC 169

QY 64 TCTGTGTCTTCTTCATGAGAGTCAAGCATATTTCAAGAACTGGAACCTGCATGC 123
 Db 190 TCTGTGTCTTCTTCATGAGAGTCAAGCATATTTCAAGAACTGGAACCTGCATGC 249

QY 124 CATTTCAAACTCTCAAAACATTAAGCTGATGAGTCTGATGATTTTGGCAGACAG 163
 Db 250 CAATTTGAAACTCTCAAAACATTAAGCTGATGAGTCTGATGATTTTGGCAGACAG 309

QY 184 GATAAGCTGTTCTGTATGATATTCAGAGCAAGAAAGCAACCTCAAAATGTTTCATCTC 243
 Db 310 GATAAGCTGTTCTGTATGATATTCAGAGCAAGAAAGCAACCTCAAAATGTTTCATCTC 369

QY 244 AAATATTAAGGCGGTACAGCTTTGACAAAGCAACTGACCTGAGACTCCACATGTT 303
 Db 370 AAATATTAAGGCGGTACAGCTTTGACAAAGCAACTGACCTGAGACTCCACATGTT 429

QY 304 CAGATCAAGCAAGGAGGACATATCAGTCTTCATTAATAAAGGCCCAAGGAGCTA 363
 Db 430 CAGATCAAGCAAGGAGGAGGACATATCAGTCTTCATTAATAAAGGCCCAAGGAGCTA 489

QY 364 GTTCCATGACCAAAATGAGTTCTGACCTATCATGCTTGTATCACTCAGTCAACCTGAA 423
 Db 490 GTTCCATGACCAAAATGAGTTCTGACCTATCATGCTTGTATCACTCAGTCAACCTGAA 549

QY 424 ATACAGTAACTTCTATATGACAGAAAATTTGGCATATTAATTTGACCTGCTATCT 483
 Db 550 ATAGTACCAATTTCTAAATATGACAGAAA--TGTGTACATTAATTTGACCTGCTATCT 606

QY 484 ATACAGTAACTTCTATATGACAGAAAATTTGGCATATTAATTTGACCTGCTATCT 543
 Db 607 ATACAGTAACTTCTATATGACAGAAAATTTGGCATATTAATTTGACCTGCTATCT 666

QY 544 ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATATATGACAGAACTGTACACGTT 603

Db 667 ATCGATATGATGATATATGACAGAAATTCAGATTAATATGACAGAACTGTACAGCTT 726
 QY 604 TCTATCAGCTTCTCTTTTTCAGTCCCTGAG--CACACATGTGAGGCTTTTGTGCC 660
 Db 727 TCCATCAGCTTCTCTTTTTCAGTCCCTGAG--CACACATGTGAGGCTTTTGTGCC 786

QY 661 CTGAACCTGAGACACTGGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
 Db 787 CTGAACCTGAGACACTGGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 837

QY 721 AAGGATTAAGAGACCTGACAAAGCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 Db 838 GAGGACCTCTCAGCTCCCTCCAGCAACATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897

QY 781 GTTGTCTTTTGTGGATGATGCTCTTTAAACACTTAAGAAAGAGAGAGAGAGAGCT 840
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QY 841 GGCCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 958 CGCACTCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017

QY 901 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
 Db 1018 AAAAGAGAAATATCATATATCATATATCATATATCATATATCATATATCATATAT 1077

QY 958 TTGAAGACAGCCTCAGCGACAAAAGTACTACATTTT 996
 Db 1078 TCGAAGACATCTTCATCGCACAAAAGTACTACATGTTTT 1116

RESULT 10
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 LOCUS HS004343
 DEFINITION Human CD86 antigen mRNA, complete cds.
 ACCESSION U04343
 VERSION U04343.1 GI:439838
 KEYWORDS B70; B7-2.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 1424)
 Azuma, M., Ito, D., Yagita, H., Okumura, K., Phillips, J.H., Lanier, L.L.
 and Somoza, C.
 B70 antigen is a second ligand for CTLA-4 and CD28
 JOURNAL Nature 366 (6450), 76-79 (1993)
 MEDLINE 94050123
 REFERENCE 2 (bases 1 to 1424)
 Fernandez-Ruiz, E., Somoza, C., Sanchez-Madrid, F., and Lanier, L.L.
 same region as CD80 (B7/B7.1) gene in human chromosome 3q13-q23
 Unpublished
 3 (bases 1 to 1424)
 Somoza, C.
 Direct Submission
 Submitted (14-DEC-1993) Chomorro Somoza, Human Immunology, DNAX
 Research Institute of Molecular and Cellular Biology, 901
 California Avenue, Palo Alto, CA 94304, USA

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 JOURNAL
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 REFERENCE
 AUTHORS
 JOURNAL

FEATURES
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Best Local Similarity	75.7%;	Pred. No. 1.	le-139;	
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DB	130	GGCATTGTGTGACAGCACATATGGGACTGTAGTAAACATTTCTCTTGTGTAGGCTCTCTGCTC	189	
QY	64	TCGAGCTTCTTCCTCAATGGAAGAGTCAAGCATATTTCACAGACCTGGAGACCTGCATC	123	
DB	190	TCGAGCTCTCTCTCTGTGAGATTCACGATTATTTTAAATGAGCTGCACACCTGCCATCC	249	
QY	124	CATTTTACAAACCTCTCAAAACATTAAGCCTGGATGACCTGGTAGTATTTTGGCAGACAG	183	
DB	250	CAATTTGCAAACTCTCAAAACCAAAACCTGAGTACCTGTAGTATTTTGGCAGACAG	309	
QY	184	GATAAGCTGGTTCTGTATGAGATATTCACAGGCAAGAAGAACCCCTCAAAATGTTATCTC	243	
DB	310	GAAACCTGGTTCTGTATGAGTATCTTAGGCAAGAAATTTTCACAGTGTATTC	369	
QY	244	AAATTAAGGGCCGTCAAGCTTTGCAAGACAACTGGACCCCTGAGCTCCACATGTT	303	
DB	370	AAATTAATGGCCGCGCAGAGTTTGTATGGACAGTTGGACCTGAGCTTACATCTT	429	
QY	304	CAGATCAAGGACAGGGCACATATCATCTGTTTCATTCAATTATTAAGGGCCCAAGGACTA	363	
DB	430	CAGATCAAGGACAGGGCTGTATCATGTATCATTCATCCACAAAAAGCCACAGGAATG	489	
QY	364	GTTCCCATGCACCAAAATGTGCTGCAATGAGCTGTGATGCTGCTGATCTCAAGTAACTGAA	423	
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QY	424	ATPACAGTACTGTATATAGAAACAGAAATTTCTGGCATCATTAATTTGACCTGCTCATCT	483	
DB	550	ATAGTACCATTTTCTAATATTAACAGAAA--TGCTGACATTAATTTGACCGCTCATCT	606	
QY	484	ATACAGGTGTACCCGGAACCTTAAGGAGTGTATTTTCAAGCTTAACAGTGAATTCACCT	543	
DB	607	ATACAGGTGTACCCGGAACCTTAAGGAGTGTATTTTCAAGCTTAACAGTGAATTCACCT	666	
QY	544	ACTAAGTATGATACGTCTATGAAGAATCTCAAAATAATGTGACAGAACTGTACACGTT	603	
DB	667	ATCGATGATGATGATGATATATGCAAAATCTCAAAATATGTGACAGAACTGTACACGTT	726	
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DB	727	TCCATCAGGTGTGCTTTTCATTTCCCTCATGTATGACCAATATGACCATCTCTGTATTT	786	
QY	661	CTGAACATGGAACACTGAGATGTGCTGCTCCCTACCTCTCAATATGATGACCAACCT	720	
DB	787	CTGGAACCTGAAA--AGACGGGCTTTTATCTTACCTTTCTCTATAG-----AGCTT	837	
QY	721	AAGGATTAAGACCTCGAACAAGGCCACTTCTCTGATGTGGGCTGTACTGTATGTTT	780	
DB	838	GAGGACCTCTAGCCCTCCCGACAGCAACATCTCTTGATATACAGCTGTACTTCCAAAGTT	897	
QY	781	GTTGTTTTTGGGATGGTGTCTCTTTAAACACTAAGGAAAAGGAAAGAGACAGCT	840	
DB	898	ATTATATGTGTGATGTTTCTGTAAATTTATGGAATGGAAGAAAGAAAGACGGCT	957	
QY	841	GGCCCTCTCATGATGTGAACATCAAAAGGAGAGAAAGAGAGCAAAACAGACAC	900	
DB	958	CGCAACTCTTTAATATGTGGAACCAACACATGTGAGAGGAGGAAGAGATGAACACCAAG	1017	
QY	901	GAAAGATGACCATTCACGCTGAGAGATCTGATGAAGCCCAAGT--TATTAACATT	957	
DB	1018	AAAAGAGAAAATTCATATACCTGGAAGATCTGATGAAGCCCAAGCTGTTTAAAGT	1077	

RESULT 6					
LOCUS	AX027016		994 bp	DNA	linear
DEFINITION	Sequence 13 from Patent WO037102.				
ACCESSION	AX027016				
VERSION	AX027016.1	GI:10188045			
KEYWORDS					
SOURCE	pig.				
ORGANISM	Sus scrofa				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
REFERENCE	1 (bases 1 to 994)				
AUTHORS	Rodgers,N.J., Dorling,A. and Lechler,R.I.				
TITLE	Immunosuppression				
JOURNAL	Patent: WO 0037102-A 13 29-JUN-2000;				
	ROGERS NICHOLA JANE (GB) ; DORLING ANTHONY (GB) ; ML LAB PLC (GB) ;				
	LECHLER ROBERT IAN (GB)				
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source	1..994				
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BASE COUNT	302 a	241 c	202 g	249 t	
ORIGIN					
	Query Match 62.5%; Score 622.8; DB 6; Length 994;				
	Best Local Similarity 80.7%; Pred.No.1,2e-158;				
	Matches 794; Conservative 0; Mismatches 172; Indels 18; Gaps 5;				
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Dd	1	ATTGGAGTAGTAACAATCTCTCTTTGTGATGGTCCTCTGCTGCTGCTCCTCTCTTG	60		
Oy	82	AAGAGTCAAGCATATTTTCAACAAGAAGCTGAGAACTGCCATGTCATTTTCAACAATCTCAA	141		
Dd	61	AAAATGTACAGCATATTTTCAATGAGACTGGAGAACTGCCATTTTCAAAATCTGCAG	120		
Oy	142	AACATAAACCCTGGATGAGCTGCTGTAATTTTGGCAGAGACAGAGATTAAGCTGTTCTGTAT	201		
Dd	121	AACCTTAACCTGGATGAGCTGCTGTAATTTTGGCAGAGACAGAGATTAAGCTGTTCTGAC	180		
Oy	202	GAGATATTCAGAGCAAGAAGAACCCCTCAAAATGTTTCATCTCAAAATATTAAGGCGCGTACA	261		
Dd	181	GAGCATATACGAGGCGCAGAGAAGAGCTCATATATGTTAATTCAGAGATATATGGGTGCACAA	240		
Oy	262	AGCTTTGACAAGGACAACACTGGAACCTGAGACTCCACATATGTTTCAGATCAAGACAAGGCG	321		
Dd	241	AGCTTTGACAAGGCGCACCTGGAGACCTGTGAGACTCCACAGTTCAAAATCAAGGACAAGGCGC	300		
Oy	322	ACATATCACTGTTTTATTCATCATATTAAGGGCCCAAGGAGCTAGTTCOCCTGACCAAAATG	381		
Dd	301	TCAATTCATATGTTTATTCATCATATAAAGGGCCGCGATGAGCTGTTCTTATTCACACGATG	360		
Oy	382	AGTTTGTGACCTATCAAGTGGCTTCTAAGCTTCAGTCAACCTGAAATVACAGTAACCTTCTAAT	441		
Dd	361	AGTTTGTGACCTATCAAGTGGCTTCTAAGCTTCAGTCAACCTGAAATVAACTACTTACTAAT	420		
Oy	442	AAGAAGAAATATTCGCGCATCAATAATTTGACCTGGTCACTATNCAAGSTTACACCAAGAA	501		
Dd	421	CACACAGAAATATTCG--TCAATTAATTTGACCTGGTCACTATNCAAGSTTACACCAAGAA	477		
Oy	502	CCTAAGGAGATGTATTTTTCAGCTAAACACTGAGAAATTCACACTAAGTATGATCTATCTGTC	561		
Dd	478	CCCGAAGAGATGTATATATGTTGCTAAATAGAAATTCAAACCACTGAGCATGATGCTGAC	537		
Oy	562	ATGAAGAAATTCAAATATATGTTGACAGAACTGTACAAAGTTTCTATCAGCTTGCCTTTT	621		
Dd	538	ATGAAGAAATTCCAAAATTAACATCAAGGAACTTAAAAATGATCAATCAGGAGTGTCTTT	597		
Oy	622	TGAGTCTCGAAGCACAACATGTGAGCGCTTTTGGCCCTGGAATGAGACACTGAGAG	681		
Dd	598	CCCATTCCTCCGAGACAATATGTGAGCATCGTCTGTGCTCTGCAACTTGAAGCCAACAG	657		
Oy	682	A---TGCTCTCTCCCTACCTTTCAATATATAGATGCACAACCTTAAGATVAAAGACCTGAA	738		

D	b658		AACAGTCCTTTTCCGCACTCCTTGTAATAATAGATTGAAGAACCACCGTAGGCACGCCCTGTGC	717
QY	739	CANGGCCACTTCCTCTGATGATTGCGGCTGTACTTGTAAATGTTTTGTTGTTTTGGGATG		798
D	718	CCAGAACACCATCCTCTGTGATGTCAGCTCTAATCTTAACAAGTGGCTGTGTGGGATG		777
QY	799	GATCTCTTTAAAACGCTAAGAAAAAGGAAGAAGACGCTGGCCCCCTCATGAAT--		856
D	778	GTCTCTCTTTGTAACTAAGNANAAGNAAGAAGACGCTGCCCCTCTAATGAATCT		837
QY	857	-GTGA AACCATCAA AAGGAGAG AAAAGAG ACAACAG ACACA GCAAG AA GA AG AT C CAT AC		915
D	838	GGTGA AACCAT CA A AAT GA TA GA CA CGA AG GCAG TGA CA MA ACT GA A A CA G A G C A -----		891
QY	916	CAGTACCTCAGAGAAGATCGATGAAGCCCAAGG---TATTAACATTTTGAAGACAGCCTCA		972
D	892	GAAGTCCAATGAACGATCTGATGATGAGCCCAAGTGTATGTATTTTAAAGACAGCCTCA		951
QY	973	GGCGACAAGACTACTACACATTTT		996
D	952	GATGACACACAGTACTACAGATTTT		975
R	E SULT 7			
L	O CUS	AFI06827	1795 bp mRNA MAM 14-DEC-1999	
I	N F I NITION	Canis familiaris truncated B7-2 protein (CD86) mRNA, complete cds.		
V	ER SI ON	AFI06827		
K	E Y W O R D S	AFI06827.1 GI:6572518		
S	U R C E	dog.		
O	R G A N I S M	Canis familiaris		
R	E F E R E N C E	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
T	I T L E	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
J	O U R N A L	New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules Immunogenetics 50 (5-6), 349-353 (1999)		
F	E A T U R E S	Immunogenetics 50 (5-6), 349-353 (1999) MEDLINE REFERENCE AUTHORS Yang,S. and Sim,G.-K. TITLE Direct Submission Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA Location/Qualifiers 1..1795 /organism="Canis familiaris" /db_xref="taxon:9615" /cell_type="peripheral blood mononuclear cells"		
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C	D S	7..849 /gene="CD86"		
3'	'UTR	/function="counter-receptor for CD28 and CD152 (CTLA4)" note="lacks transmembrane domain; alternatively spliced"		
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Db	733	ATGGAACACCAATCCCTCGATTTGGCGGCTCTCTGTAAATGTTGGCATTTGTGTGGGA	792
OY	797	TGGTGTCTTTAAAACACTAAGGAAAGAAGAACAGACAGCGCTGGCCCCCTCATGANT	856
Db	793	TGGTGTCTTTCTTAACACTAAGGAAAGAAGAACAGACAGCGCTGGCCCCCTCATGANT	852
OY	857	GTCGAACCATCAAAGGAGAGAAAAAGAGACAACAACACGACAGAGATGATACATAACC	916
Db	853	GTCGAACCAACAAGAGGAGAGAAAAAGAGACAGACAGCAAGAAAGATGACGTACAC	912
OY	917	ACGTACCTGAGAGATCTGATGAAGGCCAGTGTATTACATTTTGAAGACAGCCTCAGGC	976
Db	913	ATGGAACGGAAGATCTGATGAAGGCCAGTGTATTACATTTTGAAGACAGCCTCAGGC	972
OY	977	ACAAAAGTACTACATTTT 996	
Db	973	ACACAGTACTACACAGTTT 992	
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LOCUS	PICD86G	994 bp	mRNA linear MAM 17-JUN-1997
DEFINITION	Sus scrofa CD86 mRNA, complete cds.		
ACCESSION	L76099.1	GI:2198558	
VERSION	L76099.1	GI:2198558	
KEYWORDS	T cell costimulation.		
SOURCE	Pig.		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
	I (bases 1 to 994)		
	Maher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and		
	Bothwell,A.L.		
	Porcine endothelial CD86 is a major costimulator of xenogeneic		
	human T cells: cloning, sequencing, and functional expression in		
	human endothelial cells		
	J. Immunol. 157 (9), 3838-3844 (1996)		
TITLE	JOURNAL MEDLINE COMMENT		
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	ORRMILNLTNSTTEHDADKKSQNNITELYNYSIRVSLIPETPNVSIVCVLQSPS		
	KTLFLFSFCNIIDAKPPVQPPPHILIAALTVAIVVVGCVMSFVLLRKRKKQSPS		
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Best Local	80.7%	Pred. No. 1.2e-158:			
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				Indels	18:
				Gaps	5:
Qy	22	ATGGAGCTAGTACACACTCTCCCTGTGTGATGGGCCCTCTGCTCTGTGTCTTCTTCATG	81		
Db	1	ATGGAGCTAGTATACATCTCTTGTGTGATGGTCTCTCTCTGTGTCTCTCTCTG	60		
Qy	82	AAGATGCAAGCATATTTTCAACAAGACTGAGAACCTGCCATTTTCAAACTCTCAA	141		
Db	61	AAAAGTCAGGCAATATTTTCAATGAGACTGGAGAACTCCCGCTGCATTTTACAAACTCGCAG	120		
Qy	142	AACATTAAGCTGTGATGAGTGTGTATTTTGGCAGGACACAGATTAAGTGTGCTGTAT	201		
Db	121	AACGTAAAGCTGTATGATGAGTGTGTATTTTGGCAGGACACAGATTAAGTGTGCTGTAT	180		
Qy	202	GAGATATTTAGAGGCAAGAGAACCTCAAAATGTTTCATCTCAAAATATTAAGGCGCTACA	261		
Db	181	GAGCTATACCGAGGCGCAAGAGAGAGGCTCAATATGTTAAATCCAAAGTATATGAGTGCACA	240		
Qy	262	AGCTTTGACAAAGCAACACTGGACCCCTGGAGACTCCCAATGTTCAATATGAGGCAAGGCG	321		
Db	241	AGCTTTGACCAAGGCGCAAGGCTGGACCTGGAGACTCCCAACGTTCAATATGAGGCAAGGCG	300		
Qy	322	ACATATCACTGTTTCATTTATTAAGAGGCCCAAGGACACTAGTTCCCATGACCAAAATG	381		
Db	301	TCATATCAATGTTTCATTCATCATATTAAGGCGCGCATGAGACTGTTCCATATCCACAGATG	360		
Qy	382	AGTTTGCACCTATCACTGCTGTCTGCTCACTTCACTCAACTGGAATATACAGTAACTTCTAT	441		
Db	361	AGTTTGCACCTATCACTGCTGTCTGCTCACTTCACTCAACTGGAATATTAACCTACTTCTAT	420		
Qy	442	AGAAGAGAAATTTCTGGCATCATTAATTTGACCTGCTCATCTATATCAAGGTTATACCAGAA	501		
Db	421	CACACAGAAATTTCTG--TCATTAATTTGACCTGCTCATCTACCAAGGCTATCCACAGAA	477		
Qy	502	CCTAAGAGATATATTTTCACTAAACACTGGAATTCATCTAGTATGATATCTGTC	561		
Db	478	CCCGAGAGATATATGTTGCTAAATCGAAGAAATTCACACACCTGACACTGATGCTGAC	537		
Qy	562	ATGAGAAATTCCAAAATATATGTGACAGAACTGTAACAGTTTATGAGTGTGCTTTT	621		
Db	538	ATGAGAAATTCCAAAATATATGTGACAGAACTGTAACATGATATCATATAGGTTGCTTT	597		
Qy	622	TCAGTCCTGAGACACAAATGTGAGCGCTTTTGTGCGCTGAAACTGAGACACTGAG	681		
Db	598	CCCATCTCCCGAGAACAAATGTGAGCAATGCTGTGCTGCAACTGAGCAAGCAAG	657		
Qy	682	A---TGCTGCTCTCTCTACCTTTTCAATATATGATGACAACTTAAGAGATTAAGACCTGAA	738		
Db	658	ACATGCTTTTCTCTCTACCTTTTCAATATATGATGACAACTTAAGAGATTAAGACCTGTC	717		
Qy	739	CAAGGCACTTCTCTGATTTGCGGCTCTACTTGTAAATGTTTGTGTTTGTGGCATG	798		
Db	718	CCAGGCACTTCTCTGATTTGCGGCTCTACTTGTAAATGTTTGTGTTTGTGGCATG	777		
Qy	799	GTTGCTTTTAAACCTTAAGGAAAGAGAGAAAGACAGCTGGCCCTCTCATGAT--	856		
Db	778	GTTGCTTTTAAACCTTAAGGAAAGAGAGAAAGACAGCTGGCCCTCTCATGATGAT	837		
Qy	857	GTGAACCACTTCAAAAGGAGGAAAGAGAAAGAGCAACAGCAACGAAAGAGTACATAC	915		
Db	838	GTTGAACCACTTCAAAATGATACAGGAGGCGAGTGAACCACTTCAAGAACAGAGCA-----	891		
Qy	916	CACGTACCTGAGAGATCTGATGAAGCCCAAGT---TATTAATTTTGAACACAGCTCA	972		
Db	892	GAGTGCATGAGAGATCTGATGATGAGCCCAAGTGTATATTTTAAACACAGCTCA	951		
Qy	973	GCGGCAAAAGTACTACCATTTT	996		
Db	952	GATGACACAGTACTACCATTTT	975		

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Db 423 CTAGTTCCCATGACCAATGAGTTCTGACCTATCATGCTTGTCTAACTTCACTCAACT 482
QY 421 GAAATTAACAGTAACTTCTAATAGAACACAAAAATCTGCGATCATTAATTTGACCTGCTCA 480
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Db 483 GAAATTAACAGTAACTTCTAATAGAACACAAAAATCTGCGATCATTAATTTGACCTGCTCA 542
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QY 541 ACTACTAGTATGATACGTCTATGAGAAATCTCAAAATATATGTACAGAACTGTACAAAC 600
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QY 601 GTTCTTATACGCTTGCTCTTTTTCAGTCTCCCTGAGACACAAATGTGAGCGCTCTTTTGTGCC 660
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Db 663 GTTCTTATACGCTTGCTCTTTTTCAGTCTCCCTGAGACACAAATGTGAGCGCTCTTTTGTGCC 722
QY 661 CTGAACATGGAGACACTGGAGATGCTGCTCCCTACCTTTCATATATGATGACAAACCT 720
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Db 723 CTGAACATGGAGACACTGGAGATGCTGCTCCCTACCTTTCATATATGATGACAAACCT 782
QY 721 AAGATTAAGAACCTCTGACAAAGGCCACTTCTCTGATTTGGCGCTGTACTTTAATGTTT 780
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QY 841 GGGCCCTCATGATGATGTAACCATCAAAAAGGAGAGAAAAAGAGAAACAGACCAAC 900
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Db 903 GGGCCCTCATGATGATGTAACCATCAAAAAGGAGAGAAAAAGAGAAACAGACCAAC 962
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Db 963 GAAAGATACATACACAGTACCTAGAGATCTGATGAAGCCCACTGATTAACATTTTG 1022
QY 961 AAGACAGCTCTAGGCGACCAAAAGT 984
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Db 1023 AAGACAGCTCTAGGCGACCAAAAT 1046

RESULT 4
AF106826 1897 bp mRNA linear MAM 14-DEC-1999
LOCUS AF106826
DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
ACCESSION AF106826
VERSION AF106826.1 GI:6572516
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 1897)
Yang,S. and Sim,G.-K.
New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20093936
REFERENCE 2 (bases 1 to 1897)
AUTHORS Yang,S. and Sim,G.-K.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Port Collins, CO 80525, USA
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QY 137 CTCAAACATTAAGCCTGATGAGCTGTAGTATTTTGGCAGACCAAGATTAAGCTGTTG 196
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Db 259 GTACAGCTTTGACACAGAGACACTGACCTGAGACCTCCACATGTTCAAGTAAAGACA 318
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Db 619 CTTTTCATGCTCCCTGAGACACAAATGTAGAGCTCTTTGTGCTGCTGAACTGGAGAC 678
QY 677 TGGAGATCTGCTGCTCCCTACTCTTCAATATAGATGACAAACCTAAGATTAAGACCTG 736
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Db 679 T--GAAGCTTCCTCCCTACTCTTATATATATATGACACA--TAGAAGAACCAACCTG 732

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QY 181 CAGGATTAAGCTGGTTCTGTATGAGATATTCAGAGGCAAGAAACCCCAAAATGTTTCA 240
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QY 301 GTTCAGATCAAGGACAAAGGACATATCATCTGTTTCATTATTAAGGGCCCAAGGA 360
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QY 361 CTAGTTCCTCATGACCAAAATGAGTTCTGACCTATCATGCTTGTAACTTCAGTCAACT 420
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QY 901 GAAAGATACCATACACAGTACCTGAGAGATGATGAGAGCCAGTGTATTAACATTTT 960
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QY 961 AAGACAGCTCAGGCGCAAAAGTACTACACATTTT 996
 DB 1200 AAGACAGCTCAGGCGCAAAAGTACTACACATTTT 1235

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 LOCUS AF157827
 DEFINITION Felis catus CD86 antigen (CD86) mRNA, complete cds.
 ACCESSION AF157827
 VERSION AF157827.1 GI:5381423
 KEYWORDS
 SOURCE
 ORGANISM
 cat.
 Felis catus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 REFERENCE
 1 (bases 1 to 1138)
 Chou, I.-S., Hash, S.-M., Winslow, B.J. and Collisson, E.W.
 Sequence analyses of feline B7 costimulatory molecules
 Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
 MEDLINE 20180222
 PUBMED 10713336
 REFERENCE
 2 (bases 1 to 1138)
 Chou, I.-S., Hash, S., Winslow, B.J. and Collisson, E.W.
 Direct Submision
 Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
 University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA
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 JOURNAL
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 Matches 982; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGCAATTTGTGACAGCATATGGGAGTGCACACTCTCTCTGATGAGCCCTCTG 60
 DB 63 ATGGGCAATTTGTGACAGCATATGGGAGTGCACACTCTCTCTGATGAGCCCTCTG 122

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 DB 183 TGGCAATTTTACAACTCTCAAAACATTAAGCTGATGAGCTGTAGTATTTTGGCAGAC 242

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DEFINITION	AB030652	1270 bp	mRNA
ACCESSION	AB030652		linear
VERSION	AB030652.1		
KEYWORDS	B-lymphocyte activation antigen B7-2 (CD86).		
SOURCE	Felis catus peripheral blood mononuclear cell cDNA to mRNA.		
ORGANISM	Felis catus		
REFERENCE	Eukaryota; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
AUTHORS	1 (sites)		
TITLE	Nishimura, Y., Shimojima, M., Miyazawa, T., Sato, E., Nakamura, K., Izumiyu, Y., Ikeda, Y., Mikami, T. and Takahashi, E.		
JOURNAL	Molecular cloning of the cDNAs encoding the feline B-lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA4-g		
MEDLINE	Eur. J. Immunogenet. 27 (5-6), 427-430 (2000)		
REFERENCE	2048532		
AUTHORS	2 (bases 1 to 1270)		
TITLE	Nishimura, Y.		
JOURNAL	Submitted (31-Jul-1999) Yoshiro Nishimura, Faculty of Agriculture, The University of Tokyo, Department of Veterinary Microbiology; 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan (E-mail: yoshiro@crocos.uoc.ac.jp, Tel: +81-3-5841-5396, Fax: +81-3-5841-8184)		
COMMENT	Sequence updated (08-Jun-2000).		
FEATURES	Location/Qualifiers		
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BASE COUNT	378 a	281 c	260 g
ORIGIN	351 t		

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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Run on: October 19, 2002, 23:24:30 ; Search time 1363.8 Seconds
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Title: US-09-646-561-28

Perfect score: 996
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: gb_om: *
5: gb_ov: *
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11: gb_sts: *
12: gb_sy: *
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31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlgo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	980.8	98.5	1138	4	AF157827	Felis cat
4	784.8	78.8	1897	4	AF106826	Canis fam
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ALIGNMENTS

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LOCUS Felis catus CD86 (CD86) mRNA, complete cds.
DEFINITION AY007704
ACCESSION AY007704 GI:15418725
VERSION
KEYWORDS
SOURCE
ORGANISM

cat.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
1 (bases 1 to 2830)
AUTHORS Yang,S., Sellins,K.S., Powell,T., Stoneman,E. and Sim,G.K.
TITLE Novel transcripts encoding secreted forms of feline CD80 and CD86
costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)
MEDLINE 21390213
PUBMED 11498243
REFERENCE
2 (bases 1 to 2830)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Immunology, Heska Corporation, 1613
Prospect Parkway, Ft Collins, CO 80525, USA

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Db 508 ATTGGATCCACGATGATTCGACGTGTCAGTGTGCTAACTCAGTCGAACCTGAA 567
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? Sequence 3, Application US/08403253A
? Patent No. 6352694
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? GENERAL INFORMATION:
? APPLICANT: Jure, Carl H., Thompson, Craig B., Nabel, Gary J.
? APPLICANT: Gray, Gary S., Rennerl, Paul D.
? TITLE OF INVENTION: Methods for Selectively Stimulating Proliferation of T-Cells
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESS: LAHIVE & COCKFIELD
? STREET: 28 State Street
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/403,253A
? FILING DATE: March 10, 1995
? CLASSIFICATION: 435
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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/253,964
? FILING DATE: 3 JUNE 1994
? APPLICATION NUMBER: US 08/073,223
? FILING DATE: 4 JUNE 1993
? APPLICATION NUMBER: US 08/200,947
? FILING DATE: 23 FEB 1994
? APPLICATION NUMBER: US 07/864,805
? FILING DATE: 7 APR 1992
? APPLICATION NUMBER: US 08/247,505
? FILING DATE: 23 MAY 1994
? APPLICATION NUMBER: US 07/864,866
? FILING DATE: 7 APR 1992
? APPLICATION NUMBER: US 08/218,155
? FILING DATE: 25 MAR 1994
? APPLICATION NUMBER: US 07/864,807
? FILING DATE: 7 APR 1992
? APPLICATION NUMBER: US 07/902,467
? FILING DATE: 16 JUNE 1992
? APPLICATION NUMBER: US 07/275,433
? FILING DATE: 23 NOV 1988
?
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandiagouras, Amy E.
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: RPI-002CP2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 227-7400
? TELEFAX: (617) 742-4214
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1120 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 107..1093
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? US-08-403-253A-3
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? Query Match 55.2%; Score 463.8; DB 4; Length 1120;
? Best Local Similarity 80.5%; Pred. No. 7.7e-136;
? Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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RESULT 12
: Sequence 22, Application US/08702525
: Patent No. 6294660
: GENERAL INFORMATION:
: APPLICANT: Sharpe, Sharpe
: APPLICANT: Borriello, Francescopolo
: APPLICANT: Freeman, Gordon
: APPLICANT: Nadler, Lee
: TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 28 State Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/702,525
: FILING DATE:
: PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: US 08/205,697
: FILING DATE: 02-Mar-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Mandragoras, Amy E.
: REGISTRATION NUMBER: 36,207
: REFERENCE/DOCKET NUMBER: BWI-120CPUS
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1120 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 107..1093
: US-08-702-525-22

Query Match      55.2%; Score 463.8; DB 4; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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DB 167 TCTGGGTCGTCCTCTGAGATTCATGAGTTCATGAGTGCAGCTGCCATGC 226
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DB 347 AAGTATATGGCGCGCGCAAGCTTTCACAAACATTTGGACCTGAGATCCATAT 406
QY 301 CAGATCAAGGACAGGCTTGTATCATGTTGCTGATCAATATTTGCTGATCAAT 420
DB 407 CAGATCAAGGACAGGCTTGTATCATGTTGCTGATCAATATTTGCTGATCAAT 466
QY 361 GTTCCCATGACAGCATATTTGACCTATGACCTGCTGCTGCTGCTGCTGCTG 480
DB 467 ATTCGATCAGCAGATATTTGACCTATGACCTGCTGCTGCTGCTGCTGCTG 526
QY 421 ATATGATGATCTCTATAGAGAAATTTGCTGATCAATATTTGCTGATCAATAT 480
DB 527 ATAGTACCAATTTCTATATATACAGAAAA---TGTGATCAATATTTGCTGCTG 583
QY 481 ATACAGGTTTACCAAGCCAGAGATGATTTTGGTAAAGAACGGAATTCAGT 540
DB 584 ATACAGGTTTACCAAGCCAGAGATGATGTTTGGTAAAGAACGGAATTCAGT 643
QY 541 ACTAGTATGATCTGATGAGAAATTCATATATTTGCTGATCAATATTTGCTG 600
DB 644 ATGAGTATGATGATGATATATGCAAAATTCATGATATGCAAGAGTTCAG 703
QY 601 TCTATGAGCTTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
DB 704 TCTATGAGCTTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
QY 658 CTGCAACTGAGTCAATGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 704
DB 764 CTGCAACTGAGTCAATGAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 810

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CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPT-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-280-757B-1

Query Match 55.2%; Score 463.8; DB 3; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGTAATCTCAGATGCACTATGAGCACTGAATPAACATTTCTTTTGTGATGACCTCTGCTC 60
DB 107 ATGATGCCAGAGTGCATGAGTCAAGCTTATTTCAATGAGACTGACGACCTGCCATGCG 166
QY 61 TATGCTGCTGCTCCATGAGAGTCAAGCATTTTCAACAAGCTGAGAGACCTGCCATGCG 120
DB 167 TCTGCTGCTGCTCCTGAGAGATTCAGCTTATTTCAATGAGACTGACGACCTGCCATGCG 226
QY 121 CATTTCAAAATTTCTCAAAACATTAAGCCTGATGATGTTGGTATGTTTGGCAGGACGAC 180
DB 227 CAATTTGCAAACTCTCAAAACCAAGAGCTGATGATGATGATGATGATGATGATGATGATG 286
QY 181 GATAAGCTGCTGTGTCAGACGACTATPACAGAGGCAAGAGAACCTCAAAATGTTCAATGCG 240
DB 287 GAAAGACTGCTGTGATGAGGTACTTACTTGAAGAAATTTGACAGTGTTCATTTCC 346
QY 241 AAGATAAGGGCGGCACAAAGCTTTGACAAAGACAAATTTGACCCGAGACCTCCAAATATTT 300
DB 347 AAGTATATGGGGCGACAAAGTTTGAATCGACAGTTGACCTGAGACCTGACACTTCAATCTT 406
QY 301 CAGATCAAGGCAAGGGCTGTATCAATGTTTCCTTCATATTAAGGCGCCCAAGGACATC 360
DB 407 CAGATCAAGGCAAGGGCTGTATCAATGTTTCATATCAATCAACAAAGGCGCCCAAGGACATG 466
QY 361 GTTCCATGACGACCAAGATGATTTGACCTATCACTGCTTGTATCACTTCACTCAACCTGAA 420
DB 467 ATTCGATCCACCAAGATGATTTGAGACTGCTGCTTGTATCACTTCACTCAACCTGAA 526
QY 421 ATATGTAATCTCTAATAGAGAAATCTGSCATCATTAATTTGACCTGCTCATCC 480

DB 527 ATAGTACCMAATTTCTAATATTAACAGAAAA--TGTGATCATTAATTTGACCTGCTCATCT 583
QY 481 ATACAGGTTACCCAGAGAGAGATGATTTTGTGTAATAACCGAATTCAGT 540
DB 584 ATACAGGTTACCCAGAGAGATGATTTTGTGTAATAACCGAATTCAGT 643
QY 541 ACTAAGTATGATCTGTCATGAGAAATCTGAATAATATGTCACAGACCTCTACAGCTT 600
DB 644 ATCAGATATGATGATATATGACAGAAATCTCAAGTATATGTCACAGAACTGTACAGCTT 703
QY 601 TCTATCAGCTTCTCTCTCTGCTGCTGCTGAG--CAAGCATGAGCATCTCTGCTC 657
DB 704 TCCATCAGCTTCTCTCTCTGCTGCTGCTGAGCATATGACCATCTCTCTGATTT 763
QY 658 CTGCACTTGAATCAATGAGCTTCCCTCCCTCACTTATTAATATAGA 704
DB 764 CTGGAAGTCAAGAGCGGCTTTATCTTCACCTTCTCTATAGA 810

RESULT 11
US-08-205-697A-22
Sequence 22, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Boriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BMT-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-205-697A-22

Query Match 55.2%; Score 463.8; DB 4; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGTAATCTCAGATGCACTATGAGCACTGAATPAACATTTCTTTTGTGATGACCTCTGCTC 60
DB 107 ATGATGCCAGAGTGCATGAGTCAAGCTTATTTCAATGAGACTGACGACCTGCCATGCG 166

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Db 467 ATTGCATCCACCAGATGAATTCGTGACGTGCTGCTGCTAATCTGACGTCAACCTGAA 526
Qy 421 ATAATGTAAGTCTTAATAGAACAGAAATTCGCGCATCAATTAATTTGACCTGCTCATCC 480
Db 527 ATAGTACCAATTTCTTAATTAACAGAAA---TGCTACATAAATTTGACCTGCTCATCT 583
Qy 481 ATACAGGTTTACCCAGACCAAGAGATGATTTTGGTAAACCCAGAAATTCAGT 540
Db 584 ATACAGGTTTACCCAGACCAAGAGATGATTTTGGTAAACCCAGAAATTCAGT 643
Qy 541 ACTAATGATGATCTGTCATGAAAGAAATCTCAAAATTAATGTCACAGCTGACAACTG 600
Db 644 ATCGATATGATGATGATTTATTCAGAAATCTCAAGATTAATGTCACAGCTGACAACTG 703
Qy 601 TCTATCAGCTTGTCTTCTCAGTCCCTGAAG---CAAGCAATGAGCATCTTCTGCTC 657
Db 704 TCCATCAGCTTGTCTTCTCAGTCCCTGAATGTTAGAGCAATATACCATCTTCTGAT 763
Qy 658 CTGCAACTTGAGTCATGAAGCTTCCCTCCCTACCTTATTAATATAGA 704
Db 764 CTGGAACCTGACAGACGCGCTTTATCTTCACCTTCTCTATAGA 810
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RESULT 9

US-08-479-744A-1

Sequence 1, Application US/08479744A

Patent No. 6084067

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,744A

FILING DATE: June 7, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/280,757

FILING DATE: 26-JUL-1994

APPLICATION NUMBER: 08/109,393

FILING DATE: 28-AUG-1993

APPLICATION NUMBER: 08/101,624

FILING DATE: 26-JULY-1993

APPLICATION NUMBER: 08/147,773

FILING DATE: 3-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-004CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1120 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

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FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-479-744A-1
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Query Match 55.2%; Score 463.8; DB 3; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;
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Qy 1 ATGTATCTCAATGACATGATGAACTGATTAACATTCTTTGATGACCTCTGCTC 60
Db 107 ATGATCCCGAGTCCACATGAGGAGCTGATGAACATTCCTTTGATGAGCTTCTGCTC 166
Qy 61 TATGATGCTGCTCCATGAGACGATCATTTTCAACAAGATGAGCAAGTCCATG 120
Db 167 TCTGTGCTGCTCCTCTGAGATTTCAAGCTTATTTCAATGAGCTGACAGCTTCCATG 226
Qy 121 CATTTTCAAAATTCYCAAAACATTAAGCTTGATGATGTTGATGTTTGGACGACAG 180
Db 227 CAATTTGCAAACTCTCAAAACCAAAAGCTGATGAGCTAGTATTTTGGACGACAG 286
Qy 181 GATAAGCTGTTCTGTACGACTATACAGAGCAAGAACCTCAAAATTTTCATCGC 240
Db 287 GAAACCTGTTCTGATGAGTATTAAGTATTAAGCAAGAAATTTGACAGTTCATTC 346
Qy 241 AAGTATAAGGCGCCAGACAGCTTGGACAAAGACATTTGACACCTGACATTCATAT 300
Db 347 AAGTATATGAGGCGCCAGACAGCTTGGATGAGTTCGACAGTTCGACATTCAT 406
Qy 301 CAGATCAAGGACAAAGGCTTGTATCAATGTTTGTTCATCATTAAGGCCCCAAGAC 360
Db 407 CAGATCAAGGACAAAGGCTTGTATCAATGTTTGTTCATCATTAAGGCCCCAAG 466
Qy 361 GTTCCATGCAACGAGATTAATTCAGCTTACAGTGTCTTCACTTCACTCAACCTG 420
Db 467 ATTCGATCCACAGATTAATTCAGCTTACAGTGTCTTCACTTCACTCAACCTG 526
Qy 421 ATAATGTAAGTCTTAATAGAACAGAAATTCGCGCATCAATTAATTTGACCTGCT 480
Db 527 ATAGTACCAATTTCTTAATTAACAGAAA---TGTCACATAAATTTGACCTGCT 583
Qy 481 ATACAGGTTTACCCAGACCAAGAGATGATTTTGGTAAACCCAGAAATTCAGT 540
Db 584 ATACAGGTTTACCCAGACCAAGAGATGATTTTGGTAAACCCAGAAATTCAGT 643
Qy 541 ACTAATGATGATCTGTCATGAAAGAAATCTCAAAATTAATGTCACAGCTGACAACTG 600
Db 644 ATCGATATGATGATGATTTATTCAGAAATCTCAAGATTAATGTCACAGCTGACAACTG 703
Qy 601 TCTATCAGCTTGTCTTCTCAGTCCCTGAAG---CAAGCAATGAGCATCTTCTGCTC 657
Db 704 TCCATCAGCTTGTCTTCTCAGTCCCTGAATGTTAGAGCAATATACCATCTTCTGAT 763
Qy 658 CTGCAACTTGAGTCATGAAGCTTCCCTCCCTACCTTATTAATATAGA 704
Db 764 CTGGAACCTGACAGACGCGCTTTATCTTCACCTTCTCTATAGA 810
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RESULT 10

US-08-280-757B-1

Sequence 1, Application US/08280757B

Patent No. 6130316

GENERAL INFORMATION:

APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

APPLICANT: Gray, Gary S.

TITLE OF INVENTION: No. 6130316e1 CTLA4/CD28 Ligands and

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-101-624-1

Query Match 55.2%; Score 463.8; DB 2; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 369; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGTATCTCAGATGACATGAGTAATTAACATCTCTGTTGATGACCTCTGCTC 60
DB 107 ATGATGCCCACTGACACTATGAGCTGAGTAACATCTCTGTTGATGACCTCTGCTC 166
QY 61 TATGTCCTCTTCATGAGAGTCAAGCATTTTCAACAAGCTGAGACTGCGATCG 120
DB 167 TCTGTCCTCTCTCTGAGATTCAAGCTTATTTCAATGAGACTGACAGCTGCGATCG 226
QY 121 CATTTTCAAAATTTCTCAAAACATTAAGCTGATGAGTGTGATGTTTGGCAGACAG 180
DB 227 CAATTTCAAACTCTCAAAACCAAGCTGATGAGTGTGATGTTTGGCAGACAG 286
QY 181 GATAAGCTGCTCTGATGAGCTATACAGAGGCAAGAACCCCTCAAAATGTTCAATCGC 240
DB 287 GAAACTGCTCTGATGAGTGTATCTGATGAGCAAGAAATTTGACAGTGTCTCAATTC 346
QY 241 AAGATTAAGGGCGGCAAGACTTTGCAAAAGCAATTTGACCTGAGCTCATATATT 300
DB 347 AAGATTAAGGGCGGCAAGACTTTGATGCGACAGTTGGACCTGAGACTTCAAACTT 406
QY 301 CAGATCAAGGCAAGGGCTGTATCAATGTTTGTTCATCATTAAGGGCCCAAGAGACTC 360
DB 407 CAGATCAAGGCAAGGGCTGTATCAATGTTTGTTCATCATTAAGGGCCCAAGAGAG 466
QY 361 GTTCCCATGACCAAGATGATTTCTGACCTTCAGCTGCTTCTTAATTTCAACTGAA 420
DB 467 ATTGCGATCCACAGAGATGATTTGAACTGTCACTGCTTCACTCAACCTGAA 526
QY 421 AATATGTAATCTCTATTAAGCAAAATTTGCGCATCATTAATTTGACCTGCTCATTC 480
DB 527 ATGATACCAATTTCTATTAATTAACAGAAAA--TGTGACATTAATTTGACCTGCTCATTC 583
QY 481 ATACAGGTTACCCAGAACCAAGAGAGATGATTTTGGTAAAAACCGAAGATTCAGT 540
DB 584 ATACAGGTTACCCAGAACCAAGAGATGATGATGTTTGGTAAAGAACCAAGATTCAGT 643
QY 541 ACTAAGATGATGATCTGATGAGAGAAATCTCAAAATTAATGTCACAGACTCTCAACGTT 600
DB 644 ATCAGAGTATGATGATTAATGACAAATCTCAAGATTAATGTCACAGAGCTGACAGGTT 703
QY 601 TCTATTCAGCTGCTCTCTCTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 657
DB 704 TCCATTCAGCTGCTGCTCTCTCTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 763
QY 658 CTGCACTGTGAGTCAATGAGCTTCCCTCTCACTTATTAATTAATGA 704
DB 764 CTGCACTGTGAGTCAATGAGCTTCCCTCTCACTTATTAATTAATGA 810

RESULT 8
US-08-101-624-1
Sequence 1, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 5942607/1 CTL4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-101-624-1

Query Match 55.2%; Score 463.8; DB 2; Length 1120;
Best Local Similarity 80.5%; Pred. No. 7.7e-136;
Matches 369; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGTATCTCAGATGACATGAGTAATTAACATCTCTGTTGATGACCTCTGCTC 60
DB 107 ATGATGCCCACTGACACTATGAGCTGAGTAACATCTCTGTTGATGACCTCTGCTC 166
QY 61 TATGTCCTCTTCATGAGAGTCAAGCATTTTCAACAAGCTGAGACTGCGATCG 120
DB 167 TCTGTCCTCTCTCTGAGATTCAAGCTTATTTCAATGAGACTGACAGCTGCGATCG 226
QY 121 CATTTTCAAAATTTCTCAAAACATTAAGCTGATGAGTGTGATGTTTGGCAGACAG 180
DB 227 CAATTTCAAACTCTCAAAACCAAGCTGATGAGTGTGATGTTTGGCAGACAG 286
QY 181 GATAAGCTGCTCTGATGAGCTATACAGAGGCAAGAACCCCTCAAAATGTTCAATCGC 240
DB 287 GAAACTGCTCTGATGAGTGTATCTGATGAGCAAGAAATTTGACAGTGTCTCAATTC 346
QY 241 AAGATTAAGGGCGGCAAGACTTTGCAAAAGCAATTTGACCTGAGCTCATATATT 300
DB 347 AAGATTAAGGGCGGCAAGACTTTGATGCGACAGTGTGAGACCTGAGACTTCAATCTT 406
QY 301 CAGATCAAGGCAAGGGCTGTATGATGATGTTTGTTCATCAATAAGGGCCCAAGAGACTC 360
DB 407 CAGATCAAGGCAAGGGCTGTATGATGATGTTTGTTCATCAATAAGGGCCCAAGAGAG 466
QY 361 GTTCCCATGACCAAGATGATTTCTGACCTATGAGTGTGATGATGATGATGATGATGATG 420

ANTI-SENSE: NO
US-09-039-982A-33

Query Match 55.2%; Score 463.8; DB 4; Length 1002;
Best Local Similarity 80.5%; Pred. No. 7.3e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGATCTCAGATGACATATGAGATGATACATCTCTTTGTATGACCTCTGCTC 60
DB 7 ATGATCTCAGATGACATATGAGATGATACATCTCTTTGTATGACCTCTGCTC 66
QY 61 TATGCT 120
DB 67 TCTGCT 126
QY 121 CATTTTCAAAATTTCTCAAAACATTAAGCCTGATGAGTTGGTAGTTTGGCAGACAG 180
DB 127 CAATTTGCAAACTCTCAAAACCAAGCCTGATGAGTTAGTATTTTGGCAGACAG 186
QY 181 GATAAGCTGTTCTGTACGAGCTATACAGAGCAGAAAGAACCTCAAAATGTTCAATCC 240
DB 187 GAAACTTGGTTCTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 246
QY 241 AAGTATGAGGCGCCACAGAGTTGACAAAGACATGAGCCTGAGACCTGACATATAT 300
DB 247 AAGTATGAGGCGCCACAGAGTTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 306
QY 301 CAGATCAAGGACAAAGGCTTGTATCAATGTTTCTGATCATTAAGGCGCCAAAGGACATC 360
DB 307 CAGATCAAGGACAAAGGCTTGTATCAATGTTTCTGATCATTAAGGCGCCAAAGGACATC 366
QY 361 GTTCCCATGACCGAGATGATCTGACCTATCATGCTTGTATCAATCAATCAATCAATCA 420
DB 367 ATTGCTATCCACGAGATGATCTGACCTATCATGCTTGTATCAATCAATCAATCAATCA 426
QY 421 ATATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 427 ATATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 481 ATACAGGTTACCCAGAACCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 484 ATACAGGTTACCCAGAACCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 543
QY 541 ACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 544 ATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
QY 601 TCTATCAGCTTGTCT 657
DB 604 TCTATCAGCTTGTCT 663
QY 658 CTGCACTTGAAGTCAATGAGCTTCCCTACCTATTAATATAGA 704
DB 664 CTGCACTTGAAGTCAATGAGCTTCCCTACCTATTAATATAGA 710

RESULT 5

US-09-039-641-33
Sequence 33, Application US/09039641

Patent No. 6251627
GENERAL INFORMATION:

APPLICANT: Cai, Zeling

APPLICANT: Sprent, Jonathan

APPLICANT: Brumark, Anders

APPLICANT: Jackson, Michael

APPLICANT: Peterson, Per A

TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR

NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6251627th Wacker Drive, Suite 3000
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,641
FILING DATE: 8-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: ISRI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-09-039-641-33

Query Match 55.2%; Score 463.8; DB 4; Length 1002;
Best Local Similarity 80.5%; Pred. No. 7.3e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY 1 ATGATCTCAGATGACATATGAGATGATACATCTCTTTGTATGACCTCTGCTC 60
DB 7 ATGATCTCAGATGACATATGAGATGATACATCTCTTTGTATGAGCTTCTGCTC 66
QY 61 TATGCT 120
DB 67 TCTGCT 126
QY 121 CATTTTCAAAATTTCTCAAAACATTAAGCCTGATGAGTTGGTAGTTTGGCAGACAG 180
DB 127 CAATTTGCAAACTCTCAAAACCAAGCCTGATGAGTTAGTATTTTGGCAGACAG 186
QY 181 GATAAGCTGTTCTGTACGAGCTATACAGAGCAGAAAGAACCCCAAAATGTTCAATCC 240
DB 187 GAAACTTGGTTCTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 246
QY 241 AAGTATGAGGCGCCACAGAGTTGACAAAGACATGAGCCTGAGACCTGACATATAT 300
DB 247 AAGTATGAGGCGCCACAGAGTTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 306
QY 301 CAGATCAAGGACAAAGGCTTGTATCAATGTTTCTGATCATTAAGGCGCCAAAGGACATC 360
DB 307 CAGATCAAGGACAAAGGCTTGTATCAATGATCATCATCACAAAAGGCCACAGAGATG 366
QY 361 GTTCCCATGACCGAGATGATCTGACCTATCATGCTTGTATCAATCAATCAATCAATCAATCA 420
DB 367 ATTGCTATCCACGAGATGATCTGACCTATCATGCTTGTATCAATCAATCAATCAATCAATCA 426
QY 421 ATATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 427 ATATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY 481 ATACAGGTTACCCAGAACCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 484 ATACAGGTTACCCAGAACCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 543
QY 541 ACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 544 ATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603

OY		1	ATGATATCGAGTGCACCTATTGGAACTGAATAACAATTCCTTTTGATGACCCCTGGACTC	60
Db		7	ATGATATCCCCAGTACCTATTGGACTAGTAACATTCCTTTGTGATGCCCTTCTGCTC	66
OY		61	TATGTGCTGCTTCACATGAGAAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGC	120
Db		67	TCTGTGCTGCTGCTCGAAGATTTCAAGCTTTATTTCAATGAAGTAGCAGACCTGGCACTGC	126
OY		121	CATTTCACAAATTCCTCAAACATPAGAGCTTGATGAGTGGTGTAGTGTGTTTGGCAGACCAG	180
Db		127	CAATTTCCAAACTCTCTCAAAACCCAAGCCTAGTAGAGCTPATGATATTTTGGCAGGACAG	186
OY		181	GATAGAGCTGTTTTCTGTACGAGCTTATACAGAGGCCAAACAGAACCCCTCAAAATGTTCAATCGC	240
Db		187	GAANAAGCTTGTTTCGANTGAGAGTACTTATGGCAGAAAGAAATTTGACAGATGTTTCATGCC	246
OY		241	AAGTATPAGGGCCGACACAGCTTTGACAAAGACATTTGAGACCTTGAGACTTCATATATT	300
Db		247	AAGTATATGGGCCCACACAGTTTGTATGCGACGTGGAGACCTTGAGACTTCACAAATCTT	306
OY		301	CAGATCAAGGACCAAGGGCTTTATCATATGTTTGTATCATATAAGGGCCCAAGGACTC	360
Db		307	CAGATCAAGGACCAAGGGCTTTATCATATGATTCATTCATCACAAAAAGCCACAGAGATG	366
OY		361	GTTCCCATGACACGAGATGAATTCGTGACCTATCAGTGGTGTCTACATTCAGTCAACCTGAA	420
Db		367	ATTGCACTCCACAGATGAATTCGTGACTGTCAGTGGTGTCTACACTCAGTCAACCTGAA	426
OY		421	ATAATGATTAATTCCTATPAGAACGAGAAATTTCTGGCATTCATAAATTTGACCTGCTCATCC	480
Db		427	ATAGTACCAATTTCTTAATATPACAGAAAA--TGTGTACATAAATTTGACCTGCTCATCT	483
OY		481	ATPAGAGGTTACCCAGAAACCCAAAGAGATGTATTTTGGTAAMAAACCGAGAAATTCAGT	540
Db		484	ATPAGAGGTTACCCAGAAACCTTAAGAAGTGAAGTGTGTTTGGTAAGAACCAGAAATTCAGT	543
OY		541	ACTAAGTATGATCTGTCATGTAAGAAATCTCAAAATATATGTCACAGAACTCTACAACTT	600
Db		544	ATCGATATGATGTGATATATGCAAAATCTCAAGATATGTCACAGAACTGTAGAACTT	603
OY		601	TCTATCAGCTTGCTCCTTCTCAGTCCCTGGAAG---CAAGCAATGTGACACTTCTGTGTC	657
Db		604	TCCATCAGCTTGCTCCTTCTCAGTCCCTGGAAGTGTGACAGCAATATGACCACTTCTGTATTT	665
OY		658	CTGCAACTGTGATCANAGAGCTTCCCTCCCTACCTTATATATAGA 704	
Db		664	CTGGAACCTGACANAGAGCGGCTTTTATCTTCACCTTCTCTATAGA 710	
RESULT 2				
; Sequence 34, Application US/09039641				
; Patent No. 6251627				
GENERAL INFORMATION:				
APPLICANT: Cal, Zelig				
APPLICANT: Sprent, Jonathan				
APPLICANT: Brunmark, Anders				
APPLICANT: Jackson, Michael				
APPLICANT: Peterson, Per A				
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR				
TITLE OF INVENTION: ACTIVATION OF T-CELLS				
NUMBER OF SEQUENCES: 45				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Olson & Hiernl, Ltd.				
STREET: 20 No. 6251627th Wacker Drive, Suite 3000				
CITY: Chicago				
STATE: Illinois				
COUNTRY: USA				
ZIP: 60606				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				

	SOFTWARE:	Patentin Release #1.0, Version #1.25
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER:	US/09/039,641
	FILING DATE:	8-Mar-1995
	CLASSIFICATION:	
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Olson, Arne M.
	REGISTRATION NUMBER:	30,203
	REFERENCE/DOCKET NUMBER:	TSPR1710
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	(312) 580-1180
	TELEFAX:	(312) 580-1189
	INFORMATION FOR SEQ ID NO:	34:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	751 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	double
	TOPOLOGY:	linear
	MOLECULE TYPE:	cDNA
	HYPOTHETICAL:	NO
	ANTI-SENSE:	NO
	US-09-039-641-34	
	Query Match	55.2%; Score 463.8; DB 4; Length 751;
	Best Local Similarity	80.5%; Preq. No. 6,3e-136;
	Matches 569; Conservative	0; Mismatches 132; Indels 6; Gaps 2;
OY	1	ATGATCTCGATGCACCTATGGAGACTGTAAATCATTCCTCTTGATGACCCTCCTGCTC 60
Db	7	ATGATGCCCAAGCGACACTATGGAGCTGAGTAAATCTCTTTGATGAGCCCTTCGCTTC 66
OY	61	TATGTCCTGCTTCATGAAGAAGTCAAGCATATTTCAACAAGACTGAGAACCTCCATGC 120
Db	67	TCTGTCCTGCTCCTCTGTAAGATTCAAGCTTATTTCAATGAGACTGCGACCTGCATGC 126
OY	121	CATTTCCAATTCCTCAAAAATAGCCCTGGATGGTGGTAGTGTGTTGGCAGAGCACG 180
Db	127	CAATTTCCAACCTCTAANAACCAAAGCCGAGTGAAGTAAATTTTGGCAGACACGAG 186
OY	181	GATPAGCTGTTCTGTAGCAGCTATPACAGAGGCAAGAAACCCCTCAAAATGTTTATGCG 240
Db	187	GAAACTTGTCTGTAATGAGGATPACTTAGGCAAGAAATTTGACAGTGTTCATATCC 246
OY	241	AAGTATAAGGGCCGCAACAGCTTTGACAAAGCAATTTGACCCGAGACCTGCATATAT 300
Db	247	AAGATATGAGGCGCACAAAGTTTTGATTCGGACAGTTGGACCTGAGACCTTCACAACT 306
OY	301	CAGATCAGAGCAAGGGCTTGTATCAATGTTTCGTTCAATCAATAAAGCCCCMAAGACTC 360
Db	307	CAGATCAAGGCAAGGGCTTGTATCAATGTATATCAATCATCAAAAAAGCCACAGATG 366
OY	361	GTTCCCATGCACACAGATGAATTTGTACCTATAGTGTGCTTGTCTAATCTCAGTCMAC 420
Db	367	ATTGCATCCACAGATGAATTTGTGAAGTGTCAAGTGTGCTTGTACCTCAGTCAACCT 426
OY	421	ATAATGTAACCTCTATATAGACAGAAATTTGSCATCATAAATTTGACCTGCTCATCC 480
Db	427	ATAGTACCAATTTCTATATATACAGAAAA--TGtGTCAATTAATTTGACCTGCTCATC 483
OY	481	ATPACAGGTTACCAGAACCCAGAGAGATATTTTTTTGGTAPAAAACCGAGATTCAAGT 540
Db	484	ATPACAGGTTACCAGAACCTTAAGAGATGAGATGTTTGGTAAAGAACCAAAATTCAC 543
OY	541	ACTAAGTATGATPACTGTCATGAGAAATGCTCAAAATTAATGTACACAGAACTCTAC 600
Db	544	ATPAGATATGATGATTAATATGACGAATCTCAAGATTAATGTACACAGAGCTGTAC 603
OY	601	TCTATCAGCTTGTCCTTCAGTCCCTGAG---AAGCAATGTGAGCATCTTCTGTGTC 657
Db	604	TCCATCAGCTTGTCCTGTTCATTCCTGTAGTTACGAGCAATATGACCATCTCTGAT 663
OY	658	CTGACACTTGAGTCAATGAAGCTTCCCCTCCCTACTCTATTAATATAGA 704

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:49:49 : Search time 29.1303 Seconds
(without alignments)
7083.072 Million cell updates/sec

Title: US-09-646-561-19

Perfect score: 840

Sequence: 1 atgtatctcagatgcactat.....acaacagctactacacagttt 840

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCrUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463.8	55.2	751	4	US-09-039-982A-34
2	463.8	55.2	751	4	US-09-039-641-34
3	463.8	55.2	751	4	US-09-039-762A-34
4	463.8	55.2	1002	4	US-09-039-982A-33
5	463.8	55.2	1002	4	US-09-039-641-33
6	463.8	55.2	1002	4	US-09-039-762A-33
7	463.8	55.2	1120	2	US-08-456-104-1
8	463.8	55.2	1120	2	US-08-101-624-1
9	463.8	55.2	1120	3	US-08-479-744A-1
10	463.8	55.2	1120	3	US-08-280-757B-1
11	463.8	55.2	1120	4	US-08-205-697A-22
12	463.8	55.2	1120	4	US-08-702-525-22
13	463.8	55.2	1120	4	US-08-403-253A-3
14	463.8	55.2	1120	5	PCT-US95-02576-22
15	463.8	55.2	1161	4	US-08-205-697A-24
16	463.8	55.2	1161	4	US-08-702-525-24
17	463.8	55.2	1161	5	PCT-US95-02576-24
18	463.8	54.6	1424	5	US-09-326-186B-226
19	463.8	54.6	1428	5	PCT-US94-09642-1
20	463.8	54.0	972	4	US-08-848-760B-11
21	344.4	41.0	1151	2	US-08-456-104-3
22	344.4	41.0	1151	4	US-08-205-697A-20
23	344.4	41.0	1151	4	US-08-702-525-20
24	344.4	41.0	1151	5	PCT-US95-02576-20
25	344.4	41.0	1163	3	US-08-479-744A-22
26	344.4	41.0	1163	3	US-08-280-757B-22
27	337.2	40.1	1261	4	US-08-205-697A-12

28	337.2	40.1	1261	4	US-08-702-525-12	Sequence 12, Appl
29	337.2	40.1	1261	5	PCT-US95-02576-12	Sequence 12, Appl
30	232.4	27.7	330	3	US-08-479-744A-44	Sequence 44, Appl
31	232.4	27.7	330	3	US-08-280-757B-44	Sequence 44, Appl
32	175.2	20.9	306	3	US-08-479-744A-46	Sequence 46, Appl
33	175.2	20.9	306	3	US-08-280-757B-46	Sequence 46, Appl
34	86.4	10.3	210	4	US-08-205-697A-31	Sequence 31, Appl
35	86.4	10.3	210	4	US-08-702-525-31	Sequence 31, Appl
36	86.4	10.3	210	5	PCT-US95-02576-31	Sequence 31, Appl
37	45	5.4	195	4	US-08-205-697A-41	Sequence 41, Appl
38	45	5.4	195	4	US-08-702-525-41	Sequence 41, Appl
39	45	5.4	195	5	PCT-US95-02576-41	Sequence 41, Appl
40	34.6	4.1	492	4	US-09-328-111-335	Sequence 35, Appl
41	33.4	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
42	33	3.9	2747	2	US-08-874-347-1	Sequence 1, Appl1
43	33	3.9	2747	2	US-08-093-822-1	Sequence 1, Appl1
44	32.4	3.9	3341	2	US-08-868-577-18	Sequence 18, Appl
45	32	3.8	3095	6	5231168-1	Patent No. 5231168

ALIGNMENTS

RESULT 1
US-09-039-982A-34
; Sequence 34, Application US/09039982A
; Patent No. 6225042
; GENERAL INFORMATION:
; APPLICANT: Cal, Zelig
; APPLICANT: Sprent, Jonathan
; APPLICANT: Brummark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6225042th wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olson, Arne M.
; REGISTRATION NUMBER: 30,203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-039-982A-34

Query Match 55.2%; Score 463.8; DB 4; Length 751;
Best Local Similarity 80.5%; Pred. No. 6.3e-136;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

QY	74	CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAAGCTGCCATGCAATTTTACAATT	133
Db	255	CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAAGCTGCCATGCAATTTTACAAC	314
QY	134	CTCAAAACATAAGCCTGGATGAGTTGGTAGTGTGGTGGCAGACACAGATTAAGCTGTT	193
Db	315	CTCAAAACATAAGCCTGGATGAGTTGGTAGTGTGGTGGCAGACACAGATTAAGCTGTT	374
QY	194	TGTACGAGCTATACAGAGGCAAGAGAACCTCAAAATGTTTCATCGCAAGTATTAAGGCC	253
Db	375	TGTATGAGATATTCAGAGGCAAGAGAACCTCAAAATGTTTCATCGCAAGTATTAAGGCC	434
QY	254	GCACAAGCTTTACACAAGACATTTGGACCCCGACACGTCATTAATTCAGATCAAGACA	313
Db	435	GTACAAAGCTTTACACAAGACACCTGGACCTCGACACTCCAAATGTTTCAGATCAAGACA	494
QY	314	AGGCGTTGTATCATATGTTTCGTTCATCATAAAGGCGCCAAAGACCTGTTCCCATGCAC	373
Db	495	AGGCGCAATATCATCTGTTTCATTCATTAATAAGGCGCCAAAGACCTGTTCCCATGCAC	554
QY	374	AGATGATTTGACACTATCAGTGGCTGGTAACTTCAGTCAAGCTGAATTAATGTAAGTT	433
Db	555	AAATAGATTTGACACTATCAGTGGCTGGTAACTTCAGTCAAGCTGAATTAATGTAAGTT	614
QY	434	CTAATTAAGACAGAAAATCTGGCATCAATTAATTTGACCTGCTCATTCATCAAGGTTAC	493
Db	615	CTAATTAAGACAGAAAATCTGGCATCAATTAATTTGACCTGCTCATTCATCAAGGTTAC	674
QY	494	CAGAACCACAGAGACATGATTTTTTGGTAAAAACCGAATTCAGTACTAAGTATGATA	553
Db	675	CAGAACCACAGAGATGATTTTTTGGTAAAAACCGAATTCAGTACTAAGTATGATA	734
QY	554	CTGTCTATGAAGAAATCTCAAAATTAATGTCAAGAACCTCAACAGTTTCTATCAGCTGT	613
Db	735	CTGTCTATGAAGAAATCTCAAAATTAATGTCAAGAACCTCAACAGTTTCTATCAGCTGT	794
QY	614	CCTTCTCAGTCCCTGGAAGCAAGCATGTCAGCATCTTGTGTCTGTCGCAACTGAGTCAA	673
Db	795	CTTTCCTAGTCCCTGGAAGCAAGCATGTCAGCATCTTGTGTCTGTCGCAACTGAGTCAA	854
QY	674	T---GAAAGCTTCCTCCCTACCTATTAATTAAGAAACCAACAAAGAGGAGAGAA	725
Db	855	TGAGATGCTGCTCTCTCCCTACCTTCAATTAATTAATGATGCACAACTAAGATTAAGA	909
RESULT 14			
AA627930/C			
ID	AA627930	standard; DNA; 2830 BP.	
XX	AA627930;		
XX	AA627930;		
XX	20-DEC-1999	(first entry)	
DE	Feline B7-2 gene complementary DNA sequence.		
XX			
KM	B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;		
KM	allergic reaction; infectious disease; tumor development; feline;		
KM	graft rejection; inflammation; arthritis; atopic dermatitis; ss.		
OS	Felis catus.		
XX			
XX	WO9947558-A2.		
XX			
XX	23-SEP-1999.		
XX			
XX	19-MAR-1999; 99MO-US06187.		
XX			
XX	19-MAR-1998; 98US-0078765.		
XX	17-APR-1998; 98US-0062597.		
XX			
XX	(HESK-) HESKA CORP.		

PI	Sim G,	Yang S,	Sellins KS;
DR			
XX	WPI:	1999-571822/48.	
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for		
PT	treatment, e.g. autoimmune and atopic diseases	-	
XX			
PS	Claim 1: Page 121-123; 148pp: English.		
XX			
CC	The invention provides B7 and CTLA4 (T cell costimulatory proteins)		
CC	encoding nucleic acid molecules from dogs and cats. The proteins can be		
CC	expressed by standard recombinant methodology. The nucleic acid molecules		
CC	and the encoded proteins can be used for preventing or treating diseases,		
CC	e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor		
CC	development, graft rejection, inflammation, arthritic and atopic diseases		
CC	such as atopic dermatitis. They can be used in mammals such humans, dogs,		
CC	cats, cattle, sheep or pets. The products can also be used for detection,		
CC	diagnosis and drug screening.		
XX			
SQ	Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other:		
	Query Match	69.3%; Score 582.2; DB 20: Length 2830;	
	Best Local Similarity	89.4%; Pred. No. 1.2e-161;	
	Matches 639; Conservative	0; Mismatches 73; Indels 3; Gaps 1	
OY	14 GCACATGAGACTGATTAACATTCTCTTTGTGATGCACCCTCGCTCATGTGTCCTT	73	
Db	2636 GCACATAAGCAGAGCTACACACTCTCTTGATGGCCCCCTCGCTCGTGGTTCCT	2577	
OY	74 CCATGAAGACTCAAGCATATTTTACAAGAAGCTGAGAACCTGCCATGCTTTACAAAT	133	
Db	2576 CCATGAAGACTCAAGCATATTTTACAAGAAGCTGAGAACCTGCCATGCTTTACAACT	2517	
OY	134 CTCAAAACATMAACCCTGGATGATGTGTGTTTTGGCAGCACAGATAAGCTGGTTC	193	
Db	2516 CTCAAAACATMAACCCTGGATGATGTGTGTTTTGGCAGCACAGATAAGCTGGTTC	2457	
OY	194 TTGACAGCATATCAGAGGAAAGAACCCCTCAAATGTTTCATGCCAAGTAAAGGCC	253	
Db	2456 TTGATCAGATATTCAGAGGAAAGAACCCCTCAAATGTTTCATCCAATATAAGGGCC	2397	
OY	254 GCACAGCTTTGACAAGACAATTTGACCCTGAGACTGCATTAATTTGATCAACAGACA	313	
Db	2396 GTACAGCTTTGACAAGACAATTTGACCCTGAGACTGCATTAATTTGATCAACAGACA	2337	
OY	314 AGGGCTTTATCAATGTTTTCATCATFAAAGGCCAAAGAGACTCGTCCATGCACC	373	
Db	2336 AGGGCCACATCACTGTTTCATTCATTAFAAAGGCCAAAGAGACTCGTCCATGCACC	2277	
OY	374 AGATGATTTCTGCACATATGAGCTGCTGCATCTCAGCAACCTGAATAATGTAAGCTT	433	
Db	2276 AAATGAGTTCTGACCATATGAGCTGCTGCTACCTCAGTCAACCTGAATAATCAGTAAGCTT	2217	
OY	434 GTAATGAACAGAAAAATTCGACATCATTAATTTGACCTGCATCATCAATACAGTTACC	493	
Db	2216 GTAATGAACAGAAAAATTCGACATCATTAATTTGACCTGCATCATCAATACAGTTACC	2157	
OY	494 CAGAACCCAGAGAGATGTATTTTGTGTAACCGAGAGATTAACGACTGAATGATGATA	553	
Db	2156 CAGAACCTTAGAGAGATGTATTTTGTGTAACCGAGAGATTAACGACTGAATGATGATA	2097	
OY	554 CTGTCATGAAGAATCTCAAAATTAATGTCACAGACTGTACAGAGCTTCTCATACCTGT	613	
Db	2096 CTGTCATGAAGAATCTCAAAATTAATGTCACAGAGACTGTACAGAGCTTCTCATACCTGT	2037	
OY	614 CCTTCAGTCCCTGAGCAACAGCATGAGACATCTTGTGCTCGACACTTGAAGTCA	673	
Db	2036 CTTTTCAGTCCCTGAGCAACAGCATGAGAGCTTGTGTCCTGAACACTGGAGAC	1977	
OY	674 T---GAAGCTTCCCTGACTTATATATATGAACCAACAAGTGAGAGAA	725	
Db	1976 TGGAATGCTGCTCCCTGACTTATATATATGAACCAACAAGTAAAGAA	1922	

PT Novel feline proteins used to produce feline vaccines which prevent
PT infectious disease or to promote growth in homologous or heterologous
PT species -

Claim 6; Fig 3A; 186pp; English.

CC This is the nucleotide sequence of cDNA encoding feline CD86
CC (B7-2) ligand (see AAY32278). It was obtained following RT-PCR of
CC peripheral blood mononuclear cell mRNA and RACE-PCR. A vector
CC comprising nucleic acid encoding feline CD86 ligand or feline
CC soluble CD80 ligand is designated PSI-2#19-2/011298 (ATCC 209821).
CC The coexpression of CD86 with the costimulatory molecules CD28 (see
CC AAY32279) and a tumour antigen or an antigen from a pathogenic
CC organism has the ability to activate or enhance activation of
CC T-lymphocytes. Coexpression of CD86 with CTLA-4 (see AAY32280) has
CC the ability to regulate activation of T-lymphocytes. The invention
CC provides isolated nucleic acids encoding feline CD86 ligand,
CC feline CD80 (B7-1) ligand, feline CD28 receptor or feline CTLA-4
CC (CD152) receptor, as well as vectors comprising the nucleic acids,
CC and polypeptides encoded by the nucleic acids. It also provides
CC vaccines comprising the CD80, CD86, CD28 or CTLA-4 polypeptides and
CC further comprising immunogens derived from pathogens, especially
CC feline immunodeficiency virus (FIV), feline leukaemia virus,
CC feline infectious peritonitis virus, feline panleukopenia virus,
CC feline calicivirus, feline reovirus-3, feline rotavirus, feline
CC coronavirus, feline syncytial virus, feline sarcoma virus, feline
CC herpesvirus, feline Borna disease virus, rabies virus, chlamydia,
CC toxoplasmosis gondii, Dirofilaria immitis, or a flea, bacterial
CC pathogen, or parasite (all claimed). Vaccines capable of suppressing
CC enhancing an immune response, and vaccines capable of suppressing
CC an immune response (suitable for treating an autoimmune disease
CC or tissue or organ transplant rejection) are claimed. The
CC nucleic acids may be used for gene therapy or antisense therapy
CC protocols.

XX Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;

Query Match 69.3%; Score 582.2; DB 21; Length 1080;
Best Local Similarity 89.4%; Pred. No. 7.5e-162;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 14 GCACATGAGAACTGATATCATCTCTTTGTGATGACCCCTGCTGATAGTGGCGCTT 73
DB 79 GCACATGAGAACTGATATCATCTCTTTGTGATGACCCCTGCTGATAGTGGCGCTT 138
QY 74 CCATGAGAGTCAAGCATATTTTCAACAAGACTGAGAACTGCATGCCATTTTCAAAAT 133
DB 139 CCATGAGAGTCAAGCATATTTTCAACAAGACTGAGAACTGCATGCCATTTTCAAAAT 198
QY 134 CTCAAAACATPAGCCTGGATGAGTGTGTTGGTGGAGACCAAGCATPAGCTGTTTC 193
DB 199 CTCAAAACATPAGCCTGGATGAGTGTGTTGGTGGAGACCAAGCATPAGCTGTTTC 258
QY 194 TGTGAGGCTATATGAGGCAAGGCAAGACCTCAAAATGTTCAATGCAATPAGGGCC 253
DB 259 TGTGAGGCTATATGAGGCAAGGCAAGACCTCAAAATGTTCAATPAGGGCC 318
QY 254 GCACAGCTTTGACAAAGACATTTGACCCCTGAGACTCATATATTTTCAAGTCAAGGACA 313
DB 319 GTACAAAGCTTTGACAAAGACATTTGACCCCTGAGACTCATATATTTTCAAGTCAAGGACA 378
QY 314 AGGCTGTATCATGTTTGTGTTATCATATAAGGGCCCAAGAGCATGTTCCATGACCC 373
DB 379 AGGCTGTATCATGTTTGTGTTATCATATAAGGGCCCAAGAGCATGTTCCATGACCC 438
QY 374 AGATGAATTTGACATATCATGTTGTGTTATCATGTTCAACCAAGTATGATGACTT 433
DB 439 AATGAGTTTGTGACATATCATGTTGTGTTATCATGTTCAACCAAGTATGATGACTT 498
QY 434 CTATATGAGAAAGAAATTTGTCGATCATTAATTTGACCTGCTCATCATCAAGGTTACC 493
DB 499 CTATATGAGAAAGAAATTTGTCGATCATTAATTTGACCTGCTCATCATCAAGGTTACC 558

QY 494 CAGAACCAAGAGATGATATTTTGGTAAACCCGAGAAATTCAGTACATGATGATA 553
DB 559 CAGAACCAAGAGATGATATTTTGGTAAACCCGAGAAATTCAGTACATGATGATA 618
QY 554 CTGTATGAGAAATTTGCAAAATATATGTCACAGACTCTCAACGTTTCTATGAGCTTGT 613
DB 619 CTGTATGAGAAATTTGCAAAATATATGTCACAGACTCTCAACGTTTCTATGAGCTTGT 678
QY 614 CCTTCTGAGTCCCGAAGCAAGATGAGACATCTTGTGCTGCAACTGATGATCA 673
DB 679 CTTTTCAGTCCCTGAGACACACATGTGAGCGTCTTTTGTGCTTAAACTGAGACAC 738
QY 674 T---GAGCTTCCCTCCCTACCTTATATATATGAAACCAAGTGGAGAGAAA 725
DB 739 TGGAGATGCTGCTGCTCCCTACCTTCAATATATGATGCAACCAAGTAAAGAA 793

RESULT 13

AAZ27929
ID AAZ27929 standard; DNA; 2830 BP.

XX AAZ27929;

XX 20-DEC-1999 (first entry)

XX Feline B7-2 protein encoding DNA.

XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
XX allergic reaction; infectious disease; tumor development; feline;
XX graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX Fells catus.

XX WO947558-A2.

XX 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

XX 19-MAR-1998; 98US-0078765.

XX 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Sellins KS;

XX WPI; 1999-571822/48.

XX P-PSDB; AAY41079.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
XX treating, e.g. autoimmune and atopic diseases -

XX Claim 1; Page 116-119; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

XX Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;

Query Match 69.3%; Score 582.2; DB 20; Length 2830;
Best Local Similarity 89.4%; Pred. No. 1.2e-161;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 14 GCACATGAGAACTGATATCATCTCTTTGTGATGACCCCTGCTGATAGTGGCGCTT 73
DB 195 GCACATGAGAACTGATATCATCTCTTTGTGATGACCCCTGCTGATAGTGGCGCTT 254

XX	Feline CD86 (B7-2) cDNA.
DE	
XX	
KW	CD86; B7-2; feline; cat; recombinant virus; vaccine;
XO	immunomodulator; tumour; cancer; therapy; ss.
OS	
XX	felis domesticus.
FN	
FT	Location/Qualifiers
ET	CDS 63..1052 /*tag= a
XX	
M9	m09957295-AI.
NN	
PD	11-NOV-1999.
XX	
PX	30-APR-1999; 99WO-US09504.
PR	01-MAY-1998; 98US-0071711.
PA	(SCHE) SCHERING-PLOUGH LTD. (SCHE) SCHERING-PLOUGH VETERINARY CORP.
PI	Winslow BJ, Cochran MD:
DR	WPJ: 2000-062155/05. P-PSDB: AAY32285.
PT	Novel recombinant virus useful as immunomodulators, particularly in vaccines -
PS	Disclosure; Fig 3A; 230pp; English.
CC	This is the nucleotide sequence of cDNA coding for feline CD86 (B7-2). The cDNA was isolated from feline peripheral blood mononuclear cell cDNA by PCR. Manipulating the expression of CD28 or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC	regulates T cell proliferation and cytokine release. The invention relates to a recombinant virus that contains at least one foreign nucleic acid, inserted into a nonessential genomic region, that encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and is expressed when the recombinant virus is introduced into a suitable host. The invention also provides: a recombinant virus further comprising a foreign nucleic acid encoding an immunogen derived from a feline pathogen; recombinant viruses capable of enhancing an immune response to protect against disease; recombinant viruses expressing antisense sequences,
CC	capable of suppressing an immune response in a feline, e.g. for treatment of autoimmune disease or transplant rejection; and recombinant viruses expressing DNA encoding CD80 and/or CD86 used to reduce or eliminate a tumour in cats.
CC	
SQ	Sequence 1080 BP; 333 A; 233 C; 225 G; 279 T; 0 other;
D1	
Query Match	69.3%; Score 582.2; DB 21; Length 1080; Best Local Similarity 89.4%; Pred. No. 7.5e+12;
Matches 639;	Conservative 0; Mismatches 73; Indels 3; Gaps
OY	14 GCATGATGAAGCAATAACATTCTTGTGGATGACCCTCGTCGTAGTGACTGCTTT Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
D1	79 GCACATGAGGAGCATGAGCACACCTCCTTGTAATGGCCCCCTCGTCGTGGTTTTCTT Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
OY	74 CCATGAAGAAGTCAGCATATTTTCACACAGACTGAGAACTGCCATTTTTCACAATT Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
D1	139 CGATGAAGAGGCACGATATTTTCACAAACAGGGAAGCTCCATGGCATTTTAACAAACT Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
OY	134 CTCAAAACATTAAGCCGTGATGACTTCTGTGTGTTTGGCAGACAGACATTAAGCTGTT Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
D1	199 CTCAAACATTAAGCTCGATGAGCTGTGATTTTGGCAGACAGACATTAAGCTGTT Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
OY	194 TGTAAGAGCTATTAACAGAGCAAGAACCCCTCAAAATGTTCAATCGTAGATTAAGAGCCC Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps
D1	259 TGTATGTGAGATTTCAGAGGCAAGAACCCCTCAAAATGTTCAATCGTAGATTAAGAGCCC Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps

Oy	254	GCACACAGCTTTGACAAACAGCATTTGGACCTCGAGACTCCATTAATTTGAGATTCAAAGGACA	313
Db	319	GTACAAAGCCTTTGACAAAGGACACCTGGACCTCGAGACTCCACATGTTGAGATTCAAAGGACA	378
Oy	314	AGGACCTTGATCAATGTTTCGTTGATCATATAAAGGGCCCAAAGGACTCGTCCATGCAACC	373
Db	379	AGGGCACAATATACACTGTTTTCATCATTTATATAAGGGCCCAAAGGACACTAGTCCATGCACC	438
Oy	374	AGATGATTTCTGACCTATACAGTGGCTGTGTAACCTCACTGACCACTGAATTAATGGAACCTT	433
Db	439	AAATGAGTTCTGACCTATACAGTGGCTGTGTAACCTCACTGACCACTGAATTAATGGAACCTT	498
Oy	434	CTAATGAGACAGAAAATTTCTGGCATCATAAATTTGACCTGCTCATTCATACAGGTTAAC	493
Db	499	CTATATGAAACAGAAAATTTCTGGCATCATAAATTTGACCTGCTCATTCATACAGGTTAAC	558
Oy	494	CAGAACCCAAAGGAGATGTRATTTTTTGGTAAAAACCGAAGAAATTCAGTCAATGATGTA	553
Db	559	CAGAACCTTAAGGAGATGTRATTTTTTGGTAAAAACCGAAGAAATTCAGTCAATGATGTA	618
Oy	554	CTGTCATGAGAAATCTCAAAATTAATGTCAACAGAACTTACAAAGTTTCTATCAGCTTGT	613
Db	619	CTGTCATGAGAAATCTCAAAATTAATGTCAACAGAACTTACAAAGTTTCTATCAGCTTGC	678
Oy	614	CCTTCTCAGTCCCTGAAAGCAACATGTGAGCATCTTGCTGTCCGAACGTTGAGTCAA	673
Db	679	CTTTTTCAGTCCCTGAAAGCAACATGTGAGCATCTTGCTGTCCCTGAAAGCTGAGACAC	738
Oy	674	T---GAAGCTTCCTCCCTCCTACCTTATATATAGAAACCAACAAAGTGGAGAGAA	725
Db	729	TGGAGATGCTCCTCCTCCTACCTTCAATATATAGATGACACAACTAAGATTAACGA	793
RESUIT 12			
AAZ34785			
ID	AAZ34785 standard; cDNA, 1080 BP.		
XX	AAZ34785;		
AC			
XX	15-FEB-2000 (first entry)		
DE			
XX	Cat CD86 (B7-2) cDNA.		
XX			
KW	CD86; B7-2; lymph; cat; vaccine; feline immunodeficiency virus;		
KW	FIV; feline leukemia virus; feline infectious peritonitis virus;		
KW	feline panleukopenia virus; feline calicivirus; feline reovirus-3;		
KW	feline rotavirus; feline coronavirus; feline syncytial virus;		
KW	feline sarcoma virus; feline herpesvirus; feline borna disease;		
KW	rabies virus; chlamydia; Toxoplasmosis gondii; Dirofilaria immitis;		
KW	parasite; autoimmune disease; transplant rejection; therapy; ss.		
XX			
OS	Felis domesticus.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	63..1055	
FT	/*tag= a		
XX			
XX	W09957271-AA2.		
XX			
PD	11-NOV-1999.		
XX			
PF	30-APR-1999;	99WO-US09502.	
XX			
PR	01-MAY-1998;	98US-0071699.	
XX			
PA	(TEXA) TEXAS A & M SYSTEM.		
XX			
PI	Collison EW, Hash SM, Chol I;		
XX			
DR	WPI. 2000-052972/04.		
DR	P-PSDB; AAY32278.		
XX			

XX	The invention provides B7 and CTLA4 (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating disease e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritic and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detecting diagnosis and drug screening.									
XX										
SQ	Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;									
Query Match	69.3%	Score 582.2;	DB 20;	Length 996;						
Best Local Similarity	89.4%;	Pred. No. 7.2e-162;								
Matches 639;	Conservative 0;	Mismatches 73;	Indels 3;	Gaps						
QY	14	GCACATGTGACGTGAATATACATCTCTTTTGATGACCCCTCTCTATGTGCTGCTT	73							
DB	980	GCACATGTGAGCTAGTGTCACACTCCTCTTTGATGGCCCTCTCTCTGTGTTTCTT	921							
QY	74	CCATTAAGAGTCACAGCATATTTTCAACAAGACTGAGAGACTGCCATTTTCAAAAT	133							
DB	920	CCATTAAGAGTCACAGCATATTTTCAACAAGACTGAGAGACTGCCATTTTCAAACT	861							
QY	134	CTCAAAAGATTAAGCTCGATGATGTTGTGATGTTTGGACAGACAGATTAAGCTGTTTC	193							
DB	860	CTCAAAAGATTAAGCTCGATGATGATGTTGTGATGTTTGGACAGACAGATTAAGCTGTTTC	801							
QY	194	TGTACAGCTATATACAGAGGCAAGAGAAACCTCAAATGTTTCATGCAATATTAAGGCC	255							
DB	800	TGTATGAGATATATTCAGAGGCAAGAGAAACCTCAAAGTTTCATCTCAAATTAAGGCC	741							
QY	254	GCACAGCTTTGACAAACACATTTGAGACCTCGAGACATCCATTAATTCAGATCAAGACA	313							
DB	740	GTCACAGCTTTGACAGAGACACACAGACAGACCTCGAGACTCCAAATGTTTCAGATCAAGACA	681							
QY	314	AGGCGTTGTATCATATGTTTCGTTTCATCATTAAGAGGCCAAAGACTCGTTCCATGCACC	373							
DB	680	AGGCGCATATATCATCTGTTTCATTCATTAATTAAGAGGCCAAAGACTCGTTCCATGCACC	621							
QY	374	AGATCAATTCAGCTATACAGCGCTGCTGTAATCTTCACTCACTGAAATTAATGTGACTTT	433							
DB	620	AAATAGTTTCTGACTATACAGCGCTGCTGTAATCTTCACTCACTGAAATTAATGTGACTTT	561							
QY	434	CTAATAGAAACAAGAAATTTCTGGCATCATTAATTTGACCTGCTCATTCATACAGGTTTACC	495							
DB	560	CTAATAGAAACAAGAAATTTCTGGCATCATTAATTTGACCTGCTCATTCATACAGGTTTACC	501							
QY	494	CAGAACCCACAGAGAGATGATTTTTTGGTAAAAACCGAGAAATTCAGTACTAATGATGATA	555							
DB	500	CAGAACCCTAAGAGAGATGATTTTTTGGTAAAAACCGAGAAATTCAGTACTAATGATGATA	441							
QY	554	CTGTATGAGAAAGAAATCTCAAAATATATGTGACAGAACTCTACAGGTTTCTATCAGCTTGT	613							
DB	440	CTGTATGAGAAAGAAATCTCAAAATATATGTGACAGAACTCTACAGGTTTCTATCAGCTTGT	381							
QY	614	CGTTCTCAGTCCCTGAAGCAACAATGTACAGATCTTCTGTGCTCTGCACCTTAGTCA	673							
DB	380	CGTTTTCAGTCCCTGAAGCAACAATGTAGACGTCCTTTTGTGCCCTGAAGCTGAGACAC	321							
QY	674	T---CAGGTTCCCTCCCTACCTTTAATATAGAAACCAACAAGTGGAGGAA	725							
DB	320	TGGAGATGCTGCTCCCTACCTTTCATATATAGATGACACAACTAAGGATTAAGA	266							
RESULT 11										
XX	AA234838									
XX	AA234838 standard; cDNA; 1080 BP.									
XX	AA234838;									
DT	28-FEB-2000 (first entry)									


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QY 361 GTTCCATGCACAGATGAAATTCGACCTATCGCTGCTGCTACTGACGCAACCTGAA 420
    |||||||
Db 627 GTTCCATGCACAGATGAAATTCGACCTATCGCTGCTGCTACTGACGCAACCTGAA 568
QY 421 ATATAGTAACTTCTTAATAGAACAAAATTCGCGATCATTAATTTGACCTGCTCATCC 480
    |||||||
Db 567 ATATAGTAACTTCTTAATAGAACAAAATTCGCGATCATTAATTTGACCTGCTCATCC 508
QY 481 ATACAAAGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAACCAGATTCAGT 540
    |||||||
Db 507 ATACAAAGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAACCAGATTCAGT 448
QY 541 ACTAAGTATGATTCGTCAATGAGAAATCTCAAAATATGTCACAGAACTTCAACAGTT 600
    |||||||
Db 447 ACTAAGTATGATTCGTCAATGAGAAATCTCAAAATATGTCACAGAACTTCAACAGTT 388
QY 601 TCTATCAGCTTGTCTTCTGATCGATCCGTAAGCAAGCAATGAGCAATCTGTGTCG 660
    |||||||
Db 387 TCTATCAGCTTGTCTTCTGATCGATCCGTAAGCAAGCAATGAGCAATCTGTGTCG 328
QY 661 CAACCTTGAGTCAATGAGCTTCCCTCCCTACCTTATATATAGAACCAACA 712
    |||||||
Db 327 CAACCTTGAGTCAATGAGCTTCCCTCCCTACCTTATATATAGATGACATA 276

RESULT 7
AAZ27913
ID AAZ27913 standard: DNA: 1897 BP.
XX
AC AAZ27913:
XX
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2 protein encoding DNA.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
    allergic reaction; infectious disease; tumor development; canine;
    graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999: 99WO-US06187.
XX
PR 19-MAR-1998: 98US-0078765.
XX
PR 17-APR-1998: 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
PI WPI: 1999-571822/48.
XX
DR P-PSDB: AAY41076.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
    treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1: Page 97-99; 148bp: English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
    encoding nucleic acid molecules from dogs and cats. The proteins can be
    expressed by standard recombinant methodology. The nucleic acid molecules
    and the encoded proteins can be used for preventing or treating diseases,
    e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
    development, graft rejection, inflammation, arthritis and atopic diseases
    such as atopic dermatitis. They can be used in mammals such humans, dogs,
    cats, cattle, sheep or pets. The products can also be used for detection,
    diagnosis and drug screening.
XX
XX Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other;
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Query Match 83.8%; Score 704; DB 20; Length 1897;
Best Local Similarity 99.3%; Pred. No. 9,4e-198;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATATATCTCAGATGACACTATGAACTGAATTAACATCTCTTTGTGATGACCTCTGCTC 60
    |||||||
Db 6 ATATATCTCAGATGACACTATGAACTGAATTAACATCTCTTTGTGATGACCTCTGCTC 65
QY 61 TATGTCGTGCTTCCATGASAGTCAAGCATATTTCAACAGACTGAGAGACCTGTC 120
    |||||||
Db 66 TATGTCGTGCTTCCATGASAGTCAAGCATATTTCAACAGACTGAGAGACCTGTC 125
QY 121 CATTTTACAATTTCTCAAAACATAAACCTGGATGATGATGTTGTTGGCAGAGCAG 180
    |||||||
Db 126 CATTTTACAATTTCTCAAAACATAAACCTGGATGATGATGTTGTTGGCAGAGCAG 185
QY 181 GATTAAGCTGTTCTGTATGAGCTATACAGAGCCAAAGAACCCCTCAAAATGTCATCG 240
    |||||||
Db 186 GATTAAGCTGTTCTGTATGAGCTATACAGAGCCAAAGAACCCCTCAAAATGTCATCG 245
QY 241 AAGTATTAAGGGCCGCAAGACTTTGACAAAGACAATTTGACCTGAGACTGCATATATT 300
    |||||||
Db 246 AAGTATTAAGGGCCGCAAGACTTTGACAAAGACAATTTGACCTGAGACTGCATATATT 305
QY 301 CAGATCAAGGCAAGGGCTTGTATCAATGTTTCTTCATCAAAAGGGCCCAAGAGACTC 360
    |||||||
Db 306 CAGATCAAGGCAAGGGCTTGTATCAATGTTTCTTCATCAAAAGGGCCCAAGAGACTC 365
QY 361 GTTCCATGACACAGATGAAATTCGACCTATCGCTGCTGCTACTGCAACTGAA 420
    |||||||
Db 366 GTTCCATGACACAGATGAAATTCGACCTATCGCTGCTGCTACTGCAACTGAA 425
QY 421 ATATAGTAACTTCTTAATAGAACAAAATTCGCGATCATTAATTTGACCTGCTCATCC 480
    |||||||
Db 426 ATATAGTAACTTCTTAATAGAACAAAATTCGCGATCATTAATTTGACCTGCTCATCC 485
QY 481 ATACAAAGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAACCAGAAATTCAGT 540
    |||||||
Db 486 ATACAAAGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAACCAGAAATTCAGT 545
QY 541 ACTATAGTATGATCTGTCATGAAAGAAATCTCAAAATATATGTCACAGAACTGTACAGTT 600
    |||||||
Db 546 ACTATAGTATGATCTGTCATGAAAGAAATCTCAAAATATATGTCACAGAACTGTACAGTT 605
QY 601 TCTATCAGCTTGTCTTCTGATCGATCCCTGAGCAAGCAATGTAGCATCTTGTGTCCTG 660
    |||||||
Db 606 TCTATCAGCTTGTCTTCTGATCGATCCCTGAGCAAGCAATGTAGCATCTTGTGTCCTG 665
QY 661 CAACCTTGAGTCAATGAGCTTCCCTCCCTACCTTATATATAGAACCAACA 712
    |||||||
Db 666 CAACCTTGAGTCAATGAGCTTCCCTCCCTACCTTATATATAGATGACACATA 717

RESULT 8
AAZ27914/c
ID AAZ27914 standard: DNA: 1897 BP.
XX
AC AAZ27914:
XX
DT 20-DEC-1999 (first entry)
XX
XX Canine B7-2 gene complementary DNA sequence.
XX
DE B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
    allergic reaction; infectious disease; tumor development; canine;
    graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
```


PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 XX
 PS Claim 1; Page 102-103; 148pp; English.

CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

SQ Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match	83.8%	Score 704;	DB 20;	Length 987;
Best Local Similarity	99.3%	Pred. No. 6.9e-198;		
Matches 707; Conservative	0;	Mismatches 5;	Indels 0;	Caps 0;

QY	1	ATGTATCTCAGATGACACTATGTAAGCAATTAATACATTTCTCTTTGTATGACCCCTCTGTC	60
Db	1	ATGTATCTCAGATGACACTATGTAAGCAATTAATACATTTCTCTTTGTATGACCCCTCTGTC	60
QY	61	TATGGTGTGCTTCCTCATAGATGACATGCAATTTTACAGAGACTGAGAACTGCAATGC	120
Db	61	TATGGTGTGCTTCCTCATAGATGACATGCAATTTTACAGAGACTGAGAACTGCAATGC	120
QY	121	CATTTTACAAATTTCTCAAAACATTAAGCCTGGATGAGTGTGTTTGGCAGACACAG	180
Db	121	CATTTTACAAATTTCTCAAAACATTAAGCCTGGATGAGTGTGTTTGGCAGACACAG	180
QY	181	GATTAACCTGGTCTGTACGAGCTATACAGAGGGAAGACACCTCAAAATGTTCAATGC	240
Db	181	GATTAACCTGGTCTGTACGAGCTATACAGAGGGAAGACACCTCAAAATGTTCAATGC	240
QY	241	AAGTATATAGAGGCCGCACAAAGCTTTTGACAAAGACAAATTTGAGACCTGAGACTCCATTAATTT	300
Db	241	AAGTATATAGAGGCCGCACAAAGCTTTTGACAAAGACAAATTTGAGACCTGAGACTCCATTAATTT	300
QY	301	CAGATCAAGGACAAAGGCTGTATCATATGTTTGTTTCATCATATAAGGGGCCCAAGGACTC	360
Db	301	CAGATCAAGGACAAAGGCTGTATCATATGTTTGTTTCATCATATAAGGGGCCCAAGGACTC	360
QY	361	GTTCCCATCATCACCACATGAATTTCTGACCTCTACAGTCTGCTTAAGTCAAGTCAACTGAA	420
Db	361	GTTCCCATCATCACCACATGAATTTCTGACCTCTACAGTCTGCTTAAGTCAAGTCAACTGAA	420
QY	421	ATAATGTAACCTTCTAATATAGAACAGAAATTTGCGCATATATAATTTCACTGCTCATCC	480
Db	421	ATAATGTAACCTTCTAATATAGAACAGAAATTTGCGCATATATAATTTCACTGCTCATCC	480
QY	481	ATACAAGGTTTACCAGAACCCAGAGAGATATTTTTTGGTAAAAACCGAGAAATTTCAAGT	540
Db	481	ATACAAGGTTTACCAGAACCCAGAGAGATATTTTTTGGTAAAAACCGAGAAATTTCAAGT	540
QY	541	ACTAAGTATGATATCTGTCAATGAAGAAATTCGCAAAATATATGTACAGAACTCTACACGTT	600
Db	541	ACTAAGTATGATATCTGTCAATGAAGAAATTCGCAAAATATATGTACAGAACTCTACACGTT	600
QY	601	TCTATAGAGTTTCTCTTCTACAGTCCCTCGAAGCAAGCAATGTAGAGATCTTCTGTGCTCG	660
Db	601	TCTATAGAGTTTCTCTTCTACAGTCCCTCGAAGCAAGCAATGTAGAGATCTTCTGTGCTCG	660
QY	661	CAACTTGAAGTCAATGAAAGCTTCCCTCCCTACCTTATATATATAGAAACCAACA 712	
Db	661	CAACTTGAAGTCAATGAAAGCTTCCCTCCCTACCTTATATATATAGAAACCAACA 712	

RESULT 6	
AAZ27916/c	
ID	AAZ27916 standard; DNA; 987 BP.

XX	AA27916;
AC	
XX	
DT	20-DEC-1999 (first entry)

DE Complementary strand of canine B7-2 coding sequence.

KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease
 KW allergic reaction; infectious disease; tumor development; canine;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.
XX
PN W09947558-A2.

PD	23-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06187.
XX	

PR	19-MAR-1998;	98US-0078765.
PR	17-APR-1998;	98US-0062597.
XX		
DA	(UNCLAS) UNCLAS	CONF

XX Sim G, Yang S, Sellins KS,
PI
XX
DR WPI; 1999-571822/48.

PT new isolated B- and CD4+ nucleic acid
treating, e.g. autoimmune and atopic c
XX
PS Claim 1; Page 103-104; 148pp; English

The invention provides B7 and CD14a (T cell costimulatory proteins) encoding nucleic acid molecules from dogs and cats. The proteins can be expressed by standard recombinant methodology. The nucleic acid molecules and the encoded proteins can be used for preventing or treating diseases, e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor development, graft rejection, inflammation, arthritis and atopic diseases such as atopic dermatitis. They can be used in mammals such humans, dogs, cats, cattle, sheep or pets. The products can also be used for detection, diagnosis and drug screening.

Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

Query Match	83.8%	Score 704;	DB 20;	Length 987;
Best Local Similarity	99.3%;	Pred. No. 6.9e-198;		
Matches 707; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0

QY	1	ATGATATCAGAGTGCAGTATGGAAGCTGGAATTAACATTCCTGTTTGATGACCCCTGCTGC	60
Db	987	ATGATATCAGATGCAGTATGGAAGCTGGAATTAACATTCCTGTTTGATGACCCCTGCTGC	928
QY	61	TATGTCGTGCTTCCATGAGAAGTCAGACATATTTCAACAAGACTGGAACCTGCATGC	120
Db	927	TATGTCGTGCTTCCATGAGAAGTCAGACATATTTCAACAAGACTGGAACCTGCATGC	868
QY	121	CATTTTACAATTTCTCAAAACATATAAGCTGGATGAGTGTGATGTTTGGCAGACCAAG	180
Db	867	CATTTTACAATTTCTCAAAACATATAAGCTGGATGAGTGTGATGTTTGGCAGACCAAG	808
QY	181	GATTACCTGCTTCTGTACGAGCTATACAGAGCCAAAGAGACCCCTCAAAATGTTTCATCC	240
Db	807	GATTACCTGCTTCTGTACGAGCTATACAGAGCCAAAGAGACCCCTCAAAATGTTTCATCC	748
QY	241	AAGTATTAAGGGCCGACCAAGCTTTGACAAAGACAAATTTGGACCTCGAGACTCCATTAATTT	300
Db	747	AAGTATTAAGGGCCGACCAAGCTTTGACAAAGACAAATTTGGACCTCGAGACTCCATTAATTT	688
QY	301	CAGATCAAGGACAAAGGCGCTTGTATCATGTTTCTTTCATCATTAAGGGCCCAAGGACTC	360
Db	687	CAGATCAAGGACAAAGGCGCTTGTATCATGTTTCTTTCATCATTAAGGGCCCAAGGACTC	628

QY 781 GAAGCCAGTGTGTTAAACATTTCGAAGACAGCTTCAGCGACAAACAGTACTACAGATT 840
|||||
Db 787 GAAGCCAGTGTGTTAAACATTTCGAAGACAGCTTCAGCGACAAACAGTACTACAGATT 846

RESULT 4
AAZ27922/c
ID AAZ27922 standard; DNA: 1795 BP.

XX AAZ27922;

XX 20-DEC-1999 (first entry)

XX Canine B7-2S gene complementary DNA sequence.

XX B7: CTLA4: T cell costimulatory protein: dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX OS Canis familiaris.

XX PN WO947558-A2.

XX PD 23-SEP-1999.

XX PF 19-MAR-1999; 99WO-US06187.

XX PR 19-MAR-1998; 98US-0078765.

XX PR 17-APR-1998; 98US-0062597.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Sellins KS;

XX PI WPI: 1999-571822/48.

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -

PS Claim 1: Page 112-114; 148pp; English.

XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.

SO Sequence 1795 BP; 490 A; 347 C; 366 G; 592 T; 0 other;

Query Match 100.0%; Score 840; DB 20; Length 1795;

Best Local Similarity 100.0%; Pred. No. 5; 6e-238;

Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTATCTCAGATGACACTGTGAGCTGAATTAACATTCCTTGTGAGCCCTGCTGCTC 60
|||||

Db 1789 ATGTATCTCAGATGACACTGTGAGCTGAATTAACATTCCTTGTGAGCCCTGCTGCTC 1730

QY 61 TATGTCCTGCTTCCATGCAAGAGTCAGCATATTTTCAACAAGACTGAGAGATGCCATGC 120
|||||

Db 1729 TATGTCCTGCTTCCATGCAAGAGTCAGCATATTTTCAACAAGACTGAGAGATGCCATGC 1670

QY 121 CATTTTACAATTCGCAAAAGCATAGCCTGATGATGTTGGTGTGTTTGGCAGGACGAG 180
|||||

Db 1669 CATTTTACAATTCGCAAAAGCATAGCCTGATGATGTTGGTGTGTTTGGCAGGACGAG 1610

QY 181 GATTAAGCTGTTCTGTAGAGCTATACAGAGGCAAGAAACCTCAAAAATGTTTCATGCG 240
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Db 1609 GATTAAGCTGTTCTGTAGAGCTATACAGAGGCAAGAAACCTCAAAAATGTTTCATGCG 1550

QY 241 AAGTATPAGGGCCGACAGCTTTTGACAAAGACATTTGGACCTGAGACTCCATATATAT 300
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Db 1349 AAGTATPAGGGCCGACAGCTTTTGACAAAGACATTTGGACCTGAGACTCCATATATAT 1490

QY 301 CAGATCAGAGCAGAGGGCTTGTATCAATGTTTGGTTCATCATTAAGGCCCAAGGACCTC 360
|||||

Db 1489 CAGATCAGAGCAGAGGGCTTGTATCAATGTTTGGTTCATCATTAAGGCCCAAGGACCTC 1430

QY 361 GTTCCCATGACACAGATGAAATTCGTGACCTATGACGTGCTTGTACCTCAGTCAACCTGAA 420
|||||

Db 1429 GTTCCCATGACACAGATGAAATTCGTGACCTATGACGTGCTTGTACCTCAGTCAACCTGAA 1370

QY 421 ATAATGTAACCTTCTAAT76GAACAGAAAATTTGGCATCATTAATTTGACCTGCTCATCC 480
|||||

Db 1369 ATAATGTAACCTTCTAAT76GAACAGAAAATTTGGCATCATTAATTTGACCTGCTCATCC 1310

QY 481 ATCAAGGTTACCCAGAACCCCAAGGAGATGATTTTGGTAAACCGAATTCAGT 540
|||||

Db 1309 ATCAAGGTTACCCAGAACCCCAAGGAGATGATTTTGGTAAACCGAATTCAGT 1250

QY 541 ACTAAGTATGATCTGTCTCATGAAGAAATCTCAAAATATGTCACAGAACTCTCAAGCTT 600
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Db 1249 ACTAAGTATGATCTGTCTCATGAAGAAATCTCAAAATATGTCACAGAACTCTCAAGCTT 1190

QY 601 TCTATCAGCTTGTCTTCTCATAGTCCCTGAGCAAGCAATGTGAGCATCTGTGTCCTG 660
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Db 1189 TCTATCAGCTTGTCTTCTCATAGTCCCTGAGCAAGCAATGTGAGCATCTGTGTCCTG 1130

QY 661 CAACCTTGAATGATGAAGCTTCCCTCCCTACCTTAAATATGAAACCAACAAAGTGAAG 720
|||||

Db 1129 CAACCTTGAATGATGAAGCTTCCCTCCCTACCTTAAATATGAAACCAACAAAGTGAAG 1070

QY 721 AGAAGAAAGATGAGCAGACCAAGAAAGATGACGTACATGGAAGGGAATCTGAT 780
|||||

Db 1069 AGAAGAAAGATGAGCAGACCAAGAAAGATGACGTACATGGAAGGGAATCTGAT 1010

QY 781 GAAGCCAGTGTGTTAAACATTTCGAAGACAGCTTCAGCGACAAACAGTACTACAGATT 840
|||||

Db 1009 GAAGCCAGTGTGTTAAACATTTCGAAGACAGCTTCAGCGACAAACAGTACTACAGATT 950

RESULT 5
AAZ27915
ID AAZ27915 standard; DNA: 987 BP.

XX AAZ27915;

XX 20-DEC-1999 (first entry)

XX Canine B7-2 protein coding sequence.

DE B7: CTLA4: T cell costimulatory protein: dog; cat; autoimmune disease;

KW allergic reaction; infectious disease; tumor development; canine;

KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.

XX OS Canis familiaris.

XX PN WO947558-A2.

XX PD 23-SEP-1999.

XX PF 19-MAR-1999; 99WO-US06187.

XX PR 19-MAR-1998; 98US-0078765.

XX PR 17-APR-1998; 98US-0062597.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Sellins KS;

XX PI WPI: 1999-571822/48.

XX P-PSDB: AAY41076.

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OY 241 AAGTAAAGGGCCGACAAAGCTTTGACAAAGACAAATTGACCCCTGAGACTGCATATATT 300
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DB 600 AAGTAAAGGGCCGACAAAGCTTTGACAAAGACAAATTGACCCCTGAGACTGCATATATT 541
OY 301 CAGATCAAGGACAAAGGGTTGTATCATTGTTGCTATCATATAGAGGCCCAAGAGACAC 360
    |||
DB 540 CAGATCAAGGACAAAGGGTTGTATCATTGTTGCTATCATATAGAGGCCCAAGAGACTC 481
OY 361 GTTCCCATGACACAGATGAATTCGACCTATTCAGTGCCTTCTTAATTCAGTCAACCTGAA 420
    |||
DB 480 GTTCCCATGACACAGATGAATTCGACCTATTCAGTGCCTTCTTAATTCAGTCAACCTGAA 421
OY 421 ATAAATGTAACCTTCTTAATGAAACAAAATTCTGGCATATTAATTGACCTGCATATCC 480
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DB 420 ATAAATGTAACCTTCTTAATGAAACAAAATTCTGGCATATTAATTGACCTGCATATCC 361
OY 481 ATACAAGGTTTACCCGAAACCCAGAGAGATGATTTTGTGTAACCAAGCAATTCACAT 540
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DB 360 ATACAAGGTTTACCCGAAACCCAGAGAGATGATTTTGTGTAACCAAGCAATTCACAT 301
OY 541 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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DB 300 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 241
OY 601 TCTATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 660
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DB 240 TCTATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 181
OY 661 CAACCTGAGTCAATGAAAGCTTCCCTCTACCTTAAATATGAAACCAAGAGAGAG 720
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DB 180 CAACCTGAGTCAATGAAAGCTTCCCTCTACCTTAAATATGAAACCAAGAGAGAG 121
OY 721 AGAAAAAGAAAGTGAACAGCAAGCAAGAAAGTACGGTACCATGAACGGAAGATCTGAT 780
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DB 120 AGAAAAAGAAAGTGAACAGCAAGCAAGAAAGTACGGTACCATGAACGGAAGATCTGAT 61
OY 781 GAAGCCCAAGTGTGTAACATTTGCAAGACAGCTTCAGGCGACAAAGCTTACACAGTT 840
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DB 60 GAAGCCCAAGTGTGTAACATTTGCAAGACAGCTTCAGGCGACAAAGCTTACACAGTT 1
RESULT 3
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ID AAZ27921 standard; DNA; 1795 BP.
XX
AC AAZ27921;
DT 20-DEC-1999 (first entry)
XX
DE Canine B7-2S protein encoding DNA.
XX
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN WO947558-A2.
XX
PD 23-SEP-1999.
XX
PE 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI; 1999-571822/48.
XX
DR P-PSDB; AAY41078.
```

```
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1: Page 109-111; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
SQ Sequence 1795 BP; 592 A; 366 C; 347 G; 490 T; 0 other;
Query Match 100.0%; Score 840; DB 20; Length 1795;
Best local Similarity 100.0%; Pred. No. 5, 6e-238;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGATCTCAGATGACACTGATGAGTGAATTAATTTCTTTGTGATGACCTCTGCTC 60
    |||
DB 7 ATGATCTCAGATGACACTGATGAGTGAATTAATTTCTTTGTGATGACCTCTGCTC 66
OY 61 TATGCTGCTGCTTCATGAGAGTCAAGCATATTTCAACAAGACTGAGAGCTGCTGCTC 120
    |||
DB 67 TATGCTGCTGCTTCATGAGAGTCAAGCATATTTCAACAAGACTGAGAGCTGCTGCTC 126
OY 121 CATTTTCAAAATTTCAAAACATAAGCTGATGATGATGATGATGATGATGATGATGAT 180
    |||
DB 127 CATTTTCAAAATTTCAAAACATAAGCTGATGATGATGATGATGATGATGATGATGAT 186
OY 181 GATTAAGCTGCTCTGATGAGCTATGAGAGCAAGAAAGCAACCTCAAAATTTCAATCC 240
    |||
DB 187 GATTAAGCTGCTCTGATGAGCTATGAGAGCAAGAAAGCAACCTCAAAATTTCAATCC 246
OY 241 AAGTATTAAGGCGCGACAAAGCTTTGACAAAGACAAATTTGACCTGACATCAATATT 300
    |||
DB 247 AAGTATTAAGGCGCGACAAAGCTTTGACAAAGACAAATTTGACCTGACATCAATATT 306
OY 301 CAGATCAAGGACAAAGGGCTTGATCAATGTTGCTGATCAATTAAGAGGCCCAAGAGACTC 360
    |||
DB 307 CAGATCAAGGACAAAGGGCTTGATCAATGTTGCTGATCAATTAAGAGGCCCAAGAGACTC 366
OY 361 GTTCCCATGACACAGATGAATTCGACCTATTCAGTGCCTTCTTAATTCAGTCAACCTGAA 420
    |||
DB 367 GTTCCCATGACACAGATGAATTCGACCTATTCAGTGCCTTCTTAATTCAGTCAACCTGAA 426
OY 421 ATAAATGTAACCTTCTTAATGAAACAAAATTCTGGCATATTAATTGACCTGCATATCC 480
    |||
DB 427 ATAAATGTAACCTTCTTAATGAAACAAAATTCTGGCATATTAATTGACCTGCATATCC 486
OY 481 ATACAAGGTTTACCCGAAACCCAGAGAGATGATTTTGTGTAACCAAGCAATTCACAT 540
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DB 487 ATACAAGGTTTACCCGAAACCCAGAGAGATGATTTTGTGTAACCAAGCAATTCACAT 546
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DB 547 ACTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
OY 601 TCTATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 660
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DB 607 TCTATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 666
OY 661 CAACCTGAGTCAATGAAAGCTTCCCTCTACCTTAAATATGAAACCAAGAGAGAG 720
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DB 667 CAACCTGAGTCAATGAAAGCTTCCCTCTACCTTAAATATGAAACCAAGAGAGAG 726
OY 721 AGAAAAAGAAAGTGAACAGCAAGCAAGAAAGTACGGTACCATGAACGGAAGATCTGAT 780
    |||
DB 727 AGAAAAAGAAAGTGAACAGCAAGCAAGAAAGTACGGTACCATGAACGGAAGATCTGAT 786
```

PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
PS Claim 1; Page 114; 148bp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX
SQ Sequence 840 BP; 278 A; 181 C; 167 G; 214 T; 0 other;
Query Match 100.0%; Score 840; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.9e-238;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATCTCGATGCACTATGSAAGTAATACATTCCTTGTGATGACCCCTCCGCTC 60
DB 1 ATGATCTCGATGCACTATGSAAGTAATACATTCCTTGTGATGACCCCTCCGCTC 60
QY 61 TATGTCCTGCTTCATGGAAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGC 120
DB 61 TATGTCCTGCTTCATGGAAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGC 120
QY 121 CATTTTACAATTTCTCAAAACATTAAGCTTGATGAGTGTGTTGGCAGACCG 180
DB 121 CATTTTACAATTTCTCAAAACATTAAGCTTGATGAGTGTGTTGGCAGACCG 180
QY 181 GATAAGCTGGTTCGTACAGAGTATACAGAGCAAGCAACCTCAAAATGTTCAATC 240
DB 181 GATAAGCTGGTTCGTACAGAGTATACAGAGCAAGCAACCTCAAAATGTTCAATC 240
QY 241 AAGTAATAAGGGCCGACACAGCTTTGACAAAGACATTTGACCCCTGACCTCAATAT 300
DB 241 AAGTAATAAGGGCCGACACAGCTTTGACAAAGACATTTGACCCCTGACCTCAATAT 300
QY 301 CAGATCAAGGACAAAGGCTGTATCAATGTTGTCTATCATATAAAGCCCAAGACATC 360
DB 301 CAGATCAAGGACAAAGGCTGTATCAATGTTGTCTATCATATAAAGCCCAAGACATC 360
QY 361 GTTCCCATGACCAAGATGATTCGACCTTCAGTCTTCTCAATTCAGTCAACCTGAA 420
DB 361 GTTCCCATGACCAAGATGATTCGACCTTCAGTCTTCTCAATTCAGTCAACCTGAA 420
QY 421 AATAAGGTAACCTGTATATAGACAGAAATTTGGCATCTAATTTGACCTGCTCATCC 480
DB 421 AATAAGGTAACCTGTATATAGACAGAAATTTGGCATCTAATTTGACCTGCTCATCC 480
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QY 601 TCTATGAGCTTGTCTCTCAGTCCCTGAAGCAAGCAATGTGAGCATTTCTGTGCTG 660
DB 601 TCTATGAGCTTGTCTCTCAGTCCCTGAAGCAAGCAATGTGAGCATTTCTGTGCTG 660
QY 661 CAATTTAGATCANTGAGAGCTTCCCTCCCTACCTTATATATAGAAACCAACAAAGTGGAG 720
DB 661 CAATTTAGATCANTGAGAGCTTCCCTCCCTACCTTATATATAGAAACCAACAAAGTGGAG 720
QY 721 AGAAAGAAAGTGAAGAGCAAGCAAGAGATGAGTACATGAAAGCAAGATGTCAT 780
DB 721 AGAAAGAAAGTGAAGAGCAAGCAAGAGATGAGTACATGAAAGCAAGATGTCAT 780

QY 781 GAAGCCAGTGTGTAATCATTTCCAGACAGCTTCAGCGCAACAGTACTACAGCTT 840
DB 781 GAAGCCAGTGTGTAATCATTTCCAGACAGCTTCAGCGCAACAGTACTACAGCTT 840
RESULT 2
AAZ27924/C
ID AAZ27924 standard; DNA; 840 BP.
XX
XX AAZ27924;
AC
XX 20-DEC-1999 (first entry)
DT
XX
XX
DE Complementary strand of canine B7-2S coding sequence.
KW B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
XX
PN WO9947558-A2.
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESKA -) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
XX
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
PS
PS Claim 1; Page 115; 148bp; English.
XX
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
SQ Sequence 840 BP; 214 A; 167 C; 181 G; 278 T; 0 other;
Query Match 100.0%; Score 840; DB 20; Length 840;
Best Local Similarity 100.0%; Pred. No. 3.9e-238;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATCTCGATGCACTATGSAAGTAATACATTCCTTGTGATGACCCCTCCGCTC 60
DB 840 ATGATCTCGATGCACTATGSAAGTAATACATTCCTTGTGATGACCCCTCCGCTC 781
QY 61 TATGTCCTGCTTCATGGAAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGC 120
DB 780 TATGTCCTGCTTCATGGAAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGC 721
QY 121 CATTTTACAATTTCTCAAAACATTAAGCTTGATGAGTGTGTTGGCAGACCG 180
DB 720 CATTTTACAATTTCTCAAAACATTAAGCTTGATGAGTGTGTTGGCAGACCG 661
QY 181 GATAAGCTGGTTCGTACAGAGTATACAGAGCAAGCAAGCAACCTCAAAATGTTCAATC 240
DB 660 GATAAGCTGGTTCGTACAGAGTATACAGAGCAAGCAAGCAACCTCAAAATGTTCAATC 601

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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 126.99 Seconds

(without alignments)
11356.866 Million cell updates/sec

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Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	840	100.0	840	AAZ27923	Canine B7-2S prote
2	840	100.0	840	AAZ27924	Complementary stra
3	840	100.0	1795	AAZ27921	Canine B7-2S prote
4	840	100.0	1795	AAZ27922	Canine B7-2S gene
5	704	83.8	987	AAZ27915	Canine B7-2 protei
6	704	83.8	987	AAZ27916	Complementary stra
7	704	83.8	1897	AAZ27913	Canine B7-2 protei
8	704	83.8	1897	AAZ27914	Canine B7-2 gene c
9	582.2	69.3	996	AAZ27931	Feline B7-2 protei

C	10	582.2	69.3	996	20	AAZ27932	Complementary stra
	11	582.2	69.3	1080	21	AAZ34838	Feline CD86 (B7-2)
	12	582.2	69.3	1080	21	AAZ34785	Cat CD86 (B7-2) cD
	13	582.2	69.3	2830	20	AAZ27929	Feline B7-2 protei
C	14	582.2	69.3	2830	20	AAZ27930	Feline B7-2 gene c
	15	485	57.7	1050	21	AAZ9661	Pig costimulatory
	16	484.6	57.7	764	18	AAZ62939	Chimeric human/po
	17	463.8	55.2	831	19	AAV03230	DNA encoding CD86
	18	463.8	55.2	1120	16	AAQ81351	Human B lymphocyte
	19	463.8	55.2	1120	18	AAZ49181	Human B lymphocyte
	20	463.8	55.2	1120	20	AAV55784	Human B7-2 antigen
	21	463.8	55.2	1120	21	AAZ68409	Human B lymphocyte
	22	458.8	54.6	1424	21	AAZ29321	Human B7-2 cDNA.
	23	458.8	54.6	1428	16	AAQ85873	B70 type B antigen
	24	458.8	54.6	2205	22	AAH72616	Human cervical can
	25	453.8	54.0	738	20	AAV80293	Human B7-2 extrac
	26	453.8	54.0	738	22	AAZ89731	Nucleotide sequenc
	27	453.8	54.0	972	20	AAV83308	B7-2 cDNA. Homo s
	28	453.8	54.0	972	24	AAZ25510	Human co-stimulat
	29	344.4	41.0	1131	20	AAV55785	Mouse B7-2 antigen
	30	344.4	41.0	1153	18	AAZ49182	Mouse B lymphocyte
	31	344.4	41.0	1163	21	AAZ84050	Murine B lymphocy
	32	342.8	40.8	1163	16	AAQ81366	Murine B lymphocy
	33	337.2	40.1	1261	16	AAZ01046	Mouse B7-2 exons m
	34	317.8	37.8	942	19	AAZ99826	Rat CD86 coding se
	35	271	32.3	359	20	AAZ27935	Feline B7-2 protei
C	36	271	32.3	359	20	AAZ27936	Feline B7-2 gene (
	37	265.8	31.6	403	20	AAV89569	EST clone CR506.
	38	232.4	27.7	330	18	AAZ49197	Human B lymphocyte
	39	232.4	27.7	330	21	AAZ84082	Human B7-2 variabl
	40	218	26.0	430	21	AAZ00427	Human secreted pro
	41	175.2	20.9	306	18	AAZ49198	Human B lymphocyte
	42	175.2	20.9	306	21	AAZ84083	Human B7-2 constan
	43	169.6	20.2	509	20	AAZ27933	Feline B7-2 protei
C	44	169.6	20.2	509	20	AAZ27934	Feline B7-2 gene (
	45	86.4	10.3	210	16	AAZ01038	Human B7-2 exon 5.

ALIGNMENTS

RESULT 1	AAZ27923	standard; DNN: 840 BP.
ID	AAZ27923	
AC	AAZ27923;	
XX		
DT	20-DEC-1999 (first entry)	
XX		
DE	Canine B7-2S protein coding sequence.	
XX		
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;	
KW	allergic reaction; infectious disease; tumor development; canine;	
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.	
XX		
OS	Canis familiaris.	
XX		
PN	W09947558-A2.	
XX		
PD	23-SEP-1999.	
XX		
PF	19-MAR-1999; 99WO-US06187.	
XX		
PR	19-MAR-1998; 98US-0078765.	
PR	17-APR-1998; 98US-0062597.	
PA	(HESK-) HESKA CORP.	
XX		
PI	Sim G, Yang S, Sellins KS;	
XX		
DR	WPI; 1999-571822/48.	
XX	P-PSDB; AAY41078.	
XX		

High quality sequence stop: 400.

FEATURES

source

Location/Qualifiers

1..570

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/db_xref="taxon:9606"

/clone="IMAGE:1634297"

/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"

/lab_host="DH10B"

/note="Organ: Pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was from

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and clones: Soares NBHSF pool 1:

309384-310919, 323208-325895 Soares NB2HP pool 1:

145032-147335, 147720-148103, 148672-149255, 15002 -

150407, 151176-152327 Soares NB2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHOT

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 150 a 107 c 134 g 179 t

ORIGIN

Query Match

9.6%; Score 81; DB 9; Length 570;

Best Local Similarity 73.3%; Pred. No. 1.2e-09;

Matches 118; Conservative 0; Mismatches 40; Indels 3; Gaps 1;

```

OY 683 CCTCCCTACTTATATATAGAACCAACAAAGTGGAGAGAAAGAAAGTGAAGACCA 742
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 453 CCTCGCACTTATATATGTGACCAACATGAGAGGAGAGAGTGAACAGACCA 394
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 743 AGGAAAGAGTACGATCCATGAAGCGAAAGATCTGATGAGCCAGTGTG--TTAACA 799
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 393 AGAAAGAGAGAAAAATCCATATACCTGAAAGATGATGAAGAACCCAGCGTTTAAAA 334
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 800 TTTCGAAGACGCTCAGCGGACACACAGTACTACACAGTTT 840
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 333 GTTCGAGACATCTTCATGCGACAAAGTGAATACATGTTT 293
    |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Search completed: October 20, 2002, 04:29:47

Job time : 1010.13 secs

[illegible]

LOCUS	AM516826	496 bp	mRNA	linear	EST 03-MAR-2000
DEFINITION	xq04f01.x1 Soares_NHCC_cervical_tumor Homo sapiens CDNA clone IMAGE:2748913 3' similar to SW:CD86_HUMAN P42081 T LYMPHOCTYE ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.				
ACCESSION	AM516826				
VERSION	AM516826.1	GI:7154992			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 496) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps_email.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40UP from Gibco High quality sequence stop: 458. Location/Qualifiers				
FEATURES	source	1..496	/organism="Homo sapiens"		
		/db_xref="taxon:9606"			
		/clone="IMAGE:2748913"			
		/clone.lib="Soares_NHCC_cervical_tumor"			
		/tissue_type="tumor"			
		/lab_host="DH10B (phage-resistant)"			
		/note="Organ: cervix; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTGAGGAGCGGCCGGAACTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTR73 vector. Library is normalized; constructed by Bento Soares and M.Patima Bonaldo."			
BASE COUNT	156 a 102 c 93 g 145 t				
ORIGIN					
Query Match	10.3%; Score 86.4; DB 9; Length 496;				
Best Local Similarity	72.2%; Pred. No. 5.2e-11;				
Matches 127; conservative 0; Mismatches 46; Indels 3; Gaps 1;					
QY	668 AGTCATGAAGCTTCCTCCTACTCCTTAATVATGAAAACAACAAGTGCAGAAANG 727				
DB	204 AGAAGAAGAGGCGGCTCGCAACTCTTTATAATGTGGAACCAACCAATGTGAGAGGANG 263				
QY	728 AAAGTGACACAGCCAAAGAAAGTAGACGCTACCATGAAACGGAAGATCTGTGAAGCCC 787				
DB	264 AGAGTAACACAGCCCAAGAAAAAGAAAAATCATTAACCTTAAGATCTGTGAAGCCC 323				
QY	788 AGGTGTG---TTAACATTTCGAAGACAGCTTCAGGCGACCAACAGTACTACACAGTTT 840				
DB	324 ACGGTGTTTAAAGTTTCGAAGACATCTTCATGCGACAAAGTGATATCATGTTTTT 379				
RESULT 13					
AA946810/c	AA946810	504 bp	mRNA	linear	EST 23-JUL-1998
LOCUS	cg43c01.s1 NCI_CGAP_R1d5 Homo sapiens cDNA clone IMAGE:1589088 3'				
DEFINITION	similar to SW:CD86_HUMAN P42081 T LYMPHOCTYE ACTIVATION ANTIGEN CD86 PRECURSOR ; mRNA sequence.				
ACCESSION	AA946810				
VERSION	AA946810.1	GI:3110205			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				

ACCESSION Counter-receptor , human, mRNA sequence.
 AA056905
 VERSION AA056905.1 GI:1549545
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 REFERENCE 1 (bases 1 to 512)
 AUTHORS Tugue, C.K., Wahls, S. and Schmitz, C.
 TITLE Expressed Sequence Tags from Pig Spleen
 JOURNAL Unpublished (1996)
 COMMENT Contact: Tugue CK
 Molecular Genetics Laboratory, Department of Animal Science
 Iowa State University
 201 Kildee Hall, Ames, IA 50011-3150, USA
 Tel: 5152944252
 Fax: 5152942401
 Email: cktugue@iastate.edu
 PCR Primers
 FORWARD: TGGGAGAGACTCCTG
 BACKWARD: GACCGGCGCTCAGCT
 Insert Length: 950 Std Error: 50.00
 Seq primer: TGGGAGAGACTCCTG.
 FEATURES
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 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="SPL224"
 /clone_lib="Pig Spleen lambda gt 11 Library (Clontech Cat
 # PL1006b)"
 /tissue_type="spleen"
 /dev_stage="adult"
 /note="Oligo (drr) primed"
 BASE COUNT 125 a 106 c 114 g 163 t 4 others
 ORIGIN
 Query Match 13.8%; Score 115.8; DB 9; Length 512;
 Best Local Similarity 75.3%; Pred. No. 2.0e-18;
 Matches 171; Conservative 0; Mismatches 49; Indels 7; Gaps 2;
 QY 490 TACCCAGAACCCGAGAGATGATTTTGGTAAACCGAGATTCAGTACTAAT 549
 |||||
 DB 512 TACCCAGAACCCGAGAGATGATTTGCTAAATGCAAGATTTACACCTGAGCAT 453
 QY 550 GATCTCTGATGAGAAATCTCAAAATATGTCACAGACTCTACACGTTTCTATCAGC 609
 |||||
 DB 452 GATCTCTGATGAGAAATCTCAAAATATGTCACAGACTCTACACGTTTCTATCAGC 394
 QY 610 TTGTCTCTTCAGTCCCTGGAAGCAATGTGAGCATCTTCTGTGCTGCGCAACTTGAG 669
 |||||
 DB 393 GTGTCTCTTCCCATCCCTCCCGAGCAAAATGTGAGCATNGTCTGTGCTGCGCAACTTGAG 334
 QY 670 TCAATGAA-----GCTTCCCTCCCTTACCTTAAATATAGAAACCA 710
 |||||
 DB 333 CCAAGCAAGACACTGCTTTCTCCCTACCTTGAATATATAGTCAAA 287
 RESULT 10
 BFL171298
 LOCUS BFL171298 314 bp mRNA linear EST 23-MAR-2001
 DEFINITION PCL2416 Myeloma (PCL) cDNA library Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION BFL171298
 VERSION BFL171298.1 GI:13437512
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 314)
 AUTHORS Claudio, J.O., Tang, H., Khan, E.M., Voralia, M., Li, Z., Cukerman, E.,
 Francisco-Pabalan, O., Liew, C.C. and Stewart, A.K.

TITLE The transcriptional phenotype of myeloma cells
 JOURNAL Unpublished (2000)
 COMMENT Contact: A. Keith Stewart, M.D.
 Oncology Research
 University Health Network
 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
 Tel: (416) 946-4639
 Fax: (416) 946-6546
 Email: k.stewart@utoronto.ca
 PCR Primers
 FORWARD: 5'-GCCAAGCTCGAAATTAACCCCTGACTAAAGG-3'
 BACKWARD: 5'-CCAGTAAATGTAATACAGTACATATGAGGCG-3'
 Seq primer: 5'-GAATTAACCCCTGACTAAAGG-3'.
 FEATURES
 source
 1..314
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Myeloma (PCL) cDNA library"
 /sex="male"
 /tissue_type="Blood"
 /cell_type="Myeloma"
 /dev_stage="Plasma cell leukemia"
 /note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
 XhoI; mRNA was purified from plasma cell leukemia
 patient's peripheral blood containing >95% myeloma. An
 oligo d(T)18 primer containing XhoI restriction site was
 used to prime first strand synthesis using M-MuV reverse
 transcriptase. To protect the cDNAs from XhoI digestion in
 subsequent cloning step, the nucleotide analogue
 5-methyl-dCTP was added to the nucleotide mixture and
 1a-32P[dATP] was added to monitor the quantity and quality
 of first strand synthesis. After second-strand synthesis
 and blunting of cDNA termini, EcoRI adapters were ligated
 followed by kinase treatment and digestion with XhoI.
 The cDNAs were then size-fractionated using Sephacryl
 S-500 column and then ligated into EcoRI and XhoI digested
 Lambda Zap Express vector. The ligation product was
 packaged using Gigapack II packaging extract. The library
 had primary titre of approx. 1x10⁶. Clones from the
 primary library were randomly selected for single pass
 sequencing."

BASE COUNT 68 a 70 c 74 g 102 t
 ORIGIN
 Query Match 12.4%; Score 104.2; DB 10; Length 314;
 Best Local Similarity 77.3%; Pred. No. 1.9e-15;
 Matches 140; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 14 GCACATGGAAGTGAATACATCTCTTTGATGACCTCCTGCTATGAGTGGCTCTT 73
 |||||
 DB 125 GCACATGGAAGTGAATACATCTCTTTGATGAGCTCTCTGCTGCTGCTCTT 184
 QY 74 CCATGAAGAGTCAACATATTTCAACAAGACTGAGACTGCGCATTTTACTAATT 133
 |||||
 DB 185 CTTGTAGGATTTAAGCTTATTTAATGAGACTC---AGACCTGCAATTTTCAAACT 241
 QY 134 CTCAAAACATAGCTGTGATGAGTTGTTGGCAGAGCAGGATATGCTGTTTC 193
 |||||
 DB 242 CTCAAAACCAAGCTGAGTAGTAGTATTTTGGCAGAGCAGGAAACTGTTTC 301
 QY 194 T 194
 DB 302 T 302

RESULT 11
 AM260541
 LOCUS AM260541 380 bp mRNA linear EST 23-DEC-1999
 DEFINITION um83a03.y1 Sugano mouse liver m1a Mus musculus cDNA clone
 IMAGE:2317900 5' similar to gb:125606 Murine B7-2 mRNA, complete
 cds (MUSEF); mRNA sequence.
 ACCESSION AM260541
 VERSION AM260541.1 GI:6633522

1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH-MGC Library."

BASE COUNT 227 a 166 c 156 g 204 t
ORIGIN

Query Match 48.9%; Score 410.6; DB 10; Length 753;

Best Local Similarity 82.5%; Pred. No. 2.9e-91;

Matches 519; Conservative 0; Mismatches 104; Indels 6; Gaps 4;

```

OY 1 ATGTAATTCAGATTCGATGAGATTAACATTCCTCTGATGACCTCCTGCTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 107 ATGATGCCAGGACGACTAGGAGCTGATGATACATTCCTCTGATGACCTCCTGCTC 166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 TATGCTGCTCTCCATGAGAGTCAGCATATTCACAGACTGGAGACTGCCATGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 167 TCTGGTGTGCTCCTCTGAAAGATTCAGCTTATTCATGAGACTGACAGCTGCCATGC 226
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 CATTTTACAATTCGAAAACATTAAGCCTGATGAGTGTGTTGGGAGGACGAC 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 227 CAATTTGCAAACTCTAAAACCAAGCCTGAGTGTGATTTTGGCAGACCCAG 286
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 GATAAGCTGTTCTGTACGAGCTATACAGAGGCAAGAG-AAOCCCTCAAAATGTTTCATCG 239
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 287 GAAAGCTGTCTGTGATGAGTATCTTAGGCAAGAGAACTTGCAGAGTTCATTC 346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 240 CAAGTATAGGGCCGCAAGACTTTGACAAAGACATTTGGACCTGAGACTCCATATAT 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 347 CAAGTATAGGGCCGCAAGACTTTGATTCGAGCTGACCTGAGACTTCACATCT 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 300 TCAGATCAAGGACAGGGCTTGTATCAATGTTCTGTTCAATTAAGGGCCCAAGAGACT 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 407 TCAGATCAAGGACAGGGCTTGTATCAATGTTCTGTTCAATTAAGGGCCCAAGAGACT 466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 360 CGTTCCTGACACAGATGAAATTCGACTATGAGTGTGCTTGAAGTCAAGTCAAGCTGA 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 467 GATTCGACTCCACAGATGAAATTCGAGTGTGCTTGAAGTCAAGTCAAGTCAAGCTGA 526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 420 AATAATGTAATCTCTAATAGAACAAATTCGCGATCAATTAATTTGCTGCTCATC 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 527 AATAATGTAATCTCTAATAGAACAAATTCGCGATCAATTAATTTGCTGCTCATC 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 480 CATACAGGTTATCCAGACCAAGAGATGATTTTGTGTAAACCCAGAAATTCAG 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 TATACAGGTTATCCAGACCAAGAGATGATTTTGTGTAAACCCAGAAATTCAG 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 540 TACTAGTATGATACT-GTCAATGAGAAATCTCAAAATATGTCAGAGACTTACACAG 598
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 643 TATGAGATGATGATGATTTTATGCAAGAAATCTCAAAATATGTCAGAGACTTACACAG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 599 TTTCATCAGCTTGTCTCTCTCACTGCTCT 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 703 TTTCATCAGCTTGTCTCTCTCACTGCTCT 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 2
B1824940 655 bp mRNA linear EST 04-OCT-2001
LOCUS B1824940 60303255AF1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173789 5',
DEFINITION mRNA sequence.
ACCESSION B1824940
VERSION B1824940.1 GI:15936490
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 655)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLNL1432 row: 1 column: 14
High quality sequence start: 27
High quality sequence stop: 653.

Location/Qualifiers
1. 655

FEATURES
source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_1b="IMAGE:5173789"

/clone_1b="NIH_MGC_115"

/lab_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector:

PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH-MGC Library."

BASE COUNT 194 a 147 c 145 g 169 t
ORIGIN

Query Match 42.6%; Score 358; DB 10; Length 655;

Best Local Similarity 82.7%; Pred. No. 3e-78;

Matches 422; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

```

OY 1 ATGTAATTCAGATTCGATGAGATTAACATTCCTCTGATGAGACTCCTGCTC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 148 ATGATGCCAGGACGACTAGGAGCTGATGATACATTCCTCTGATGAGACTCCTGCTC 207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 TATGCTGCTCTCCATGAGAGTCAGCATATTCACAGACTGGAGACTGCCATGC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 208 TCTGGTGTGCTCCTCTGAAAGATTCAGCTTATTCATGAGACTGACAGCTGCCATGC 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 420 AATAATGTAATCTCTAATAGAACAAATTCGCGATCAATTAATTTGCTGCTCATC 479
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 527 AATAATGTAATCTCTAATAGAACAAATTCGCGATCAATTAATTTGCTGCTCATC 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 480 CATACAGGTTATCCAGACCAAGAGATGATTTTGTGTAAACCCAGAAATTCAG 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 584 TATACAGGTTATCCAGACCAAGAGATGATTTTGTGTAAACCCAGAAATTCAG 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 540 TACTAGTATGATACT-GTCAATGAGAAATCTCAAAATATGTCAGAGACTTACACAG 598
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 643 TATGAGATGATGATGATTTTATGCAAGAAATCTCAAAATATGTCAGAGACTTACACAG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 599 TTTCATCAGCTTGTCTCTCTCACTGCTCT 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 703 TTTCATCAGCTTGTCTCTCTCACTGCTCT 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 3

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 1001.13 Seconds
(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-19

Sequence: 1 atgatactcagatgcactat.....acaacagctactacacagttt 840

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_pln:*
15: em_gss_pln:*
16: em_gss_vitl:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	410.6	48.9	753	10	B1906246
2	358	42.6	655	10	B1824940
3	323.8	38.5	448	9	AA056906
4	281.4	33.5	629	9	BB631711
5	263.2	31.3	1002	10	BF137460
6	257.2	30.6	578	10	BM089797
7	203.6	24.2	654	9	BB635605
8	176	21.0	257	9	AA427922
9	115.8	13.8	512	9	AA056905
10	104.2	12.4	314	10	BF171298
11	99.2	11.8	380	9	AA260541
12	86.4	10.3	496	9	AA516826
13	84.8	10.1	504	9	AA946810
14	84.8	10.1	543	10	BF064222
15	81	9.6	570	9	AI093604
16	77.8	9.3	480	9	AI750143
17	73.6	8.8	347	10	BC001664

18	72.4	8.6	133	10	BF925793
19	72.4	8.6	156	10	BF925798
20	58.2	6.9	486	10	B1132458
21	50	6.0	695	10	B1767024
22	48.6	5.8	1101	12	CNS00396
23	45	5.4	391	9	AI632116
24	43	5.1	378	9	AA973397
25	40.2	4.8	393	10	BG735726
26	40.2	4.8	402	10	BG736566
27	40	4.7	1571	10	BE622476
28	39.6	4.7	1032	10	B1762625
29	39.2	4.7	317	9	BB125839
30	39.2	4.7	1101	12	CNS00F03
31	38.8	4.6	583	10	BM491628
32	38.4	4.6	211	10	BM284849
33	38.4	4.6	523	12	AA0830201
34	38.4	4.6	589	10	B1860130
35	38.2	4.5	477	12	AZ460082
36	38.2	4.5	634	10	BG986969
37	38.2	4.5	812	10	BF104731
38	38	4.5	537	12	AA065728
39	38	4.5	693	12	BH577208
40	38	4.5	735	12	BH595210
41	38	4.5	893	12	BH157217
42	38	4.5	920	12	AZ206772
43	37.8	4.5	725	9	AU120535
44	37.6	4.5	521	12	A0797471
45	37.6	4.5	848	12	AZ692617

ALIGNMENTS

RESULT 1
LOCUS B1906246 753 bp mRNA linear EST 16-OCT-2001
DEFINITION 603063172F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212648 5',
MRNA Sequence.
B1906246
VERSION B1906246.1 GI:16168907
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM1533 row: 0 column: 17
High quality sequence stop: 719.
Location/Qualifiers
1. 753
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5212648"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6, site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dt primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

FEATURES

source

Sun Oct 20 08:15:47 2002

us-09-646-561-19.rge

Page 11

Qy	658	CTGCACCTTGA	CTCATG	AGCTTCC	CTCCCA	CTTATATAT	ATAGA	704
Db	764	CTGGAAC	TGCAG	AGAGCGG	GGCTTT	ATCTT	CACCTT	TCTCTATAGA 810

Search completed: October 20, 2002, 03:16:11
Job time : 1156.19 secs

Best Local Similarity 80.5%; Pred. NO. 8.5e-113;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2.

OY 1 ATGTATCTCAGATGCACACTATGGAACCTGATAACATCTCTTTTGATGAAACCCTCGTC 60
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Db 7 ATGGATCCCAAGTGCACACTATGGGA CTGATACAATTCTCTTTTGATGAGGCCCTTCTGCTC 66

Dy 61 TATGGTGCCTCCATGAGAGTCACGATATTTCACACAGACTCGAGACTGCCATGC 12
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Db 67 TCCTGTGCTGCTCCTCTGAAGATTCACGCTTATTTCATGAGACTGCAGACCCTGCCATGC 12

Dy 121 CATTTCACAATTCACAAACATAAGCCTGATGAGTGTGGTAGTGCGAGACCAG 18
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Db 127 CAATTGGCAACTCTCAAACCCAAAGCCTGAGTGAAGTAAGTATTTTGGCAGACCCAG 18

DY 181 GATAAGCTGGTTCGTACGAGCATATACAGAGCGCAAGAGAACCCTCAAAATGTTGCATCCG 24
||| ||||||||| ||| ||||| ||||||||| | | ||||||| |
Db 187 GAAACTTGCTGTTCTGATGAGGTATACATTAGGCCAAGAGAAAATTGACACGTGTTTCATTTCC 24

Dy 241 AAGTATAAAGGGCCGCAACAGCTTTGACAAGAAGCAATTGGACCCTTGAGACTCACAATAATAT 30
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Db 247 AAGTATATAGGGCCGCAACAGTTTTGATTTCGGACAGITGGACCGTGAGACTTCACAATCTT 30

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Dy 361 GPTCCATGCACGAGAAITCTGACCATAACGTCTGGCACTTCAGTCAACTCGA 42
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 427 ATAGTACCAATTTCTAATATACAGAAA--TGCTACATTAATTGACCTGCTCATCT

481 ATACAAAGTACCCAGAACCCAGAGAGATGATTTGGTAAACCAAGATTCAGG
484 ATACACGGTACCCAGAACCTAAGAAGATGAGTGTGTTGGTAAAGACCAAGATTCACCT

544 ATCGAGTATGATGGTATTATGCGAAGTCTCAAGATTAATGTCACAGAACTGTACGACGTT 600

604 TCCATCAGCTGTCTGTTCATTCCCTGATGTTACGAGCAATATGACCATTCTTCTGATT 666

Db 664 CTGGAACTGCACAGACGGCGTTTATCTTCACCTTCTCTATAGA 710

LOCUS	1002 bp	DNA	linear	PAT 17-00
ARI60450				

ACCESSION AR160450
VERSION AR160450.1 GI:16224366
KEYWORDS

ORGANISM	REFERENCE
Unknown.	1 (bases 1 to 1002)
Unclassified.	

TITLE	Antigen presenting system and methods for activation of T-cells
JOURNAL	Patent: US 6255073-A 33 03-JUL-2001;
FEATURES	Location/Qualifiers

	/organism="unknown"							
BASE COUNT	309	a	215	c	203	g	275	t
ORIGIN								

query match	55.2%;	Score 463.8;	DB 6;	Length 1002;
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Best Local Similarity 80.5%; Pred. No. 8.5e-113;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2

Oy 1 ATGATCTCGATGCACATATGSAAGTGAATAACATTCTTTGTGATGAGACCCCTTGCTC 60
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Db 7 ATGATCCCCAGTCGACTATGGGACTGAGTAACAATCTCTTTGTGATGAGGCCCTTGCTC 66

Oy 61 TATGGTGCCTCCTCCATGAGAGTCACAGCATATTTCACACAGACTGGAGAACCTGCCATGC 12
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Db 67 TCCTGGTGCTCCTCCCTCGAAGATTCACACTTATTTCAATGAGACTCGAGACCCTGCCATGC 12

Oy 121 CATTTACAATTCACAAACATAAGCTGATGAGTGTGGTAGTGTTTTGGCAGGACCAG 18
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Dy 181 GATAGCTGGTTCGTACGAGCTATACAGAGCCCAAGAACCCCTCAAATGTTTCATCCC 24
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Db 187 GAAACTTGCTTCGAATGAGGTATACCTTAGGCCAAGAATAATTGCACAGTGTTCATTCC 24

Qy 241 AAGTATAAGGCGCACAGCTTTGACAAAGACAAATTGGACCCTGAGACTCCATAATATT 30
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Db 247 AAGTATATGGCGCGCACAGTTTGTGATTGCGACAGTGGACCCTGAGACTTCACAATCTT 30

QY 301 CAGATCAAGCACAAAGGCTTGTATCAAGTTTCGTTTCATCATAAAGGCCCAAGGACTC 36
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 Db 307 CAGATCAAGCACAAAGGCTTGTATCAAGTATTCATTCATCACAAAAGCCACAGGAATG 36
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Dy 361 GTTCCATGCACCAGAAATTCTGACCATCAGTGCTTGGTAACCTCAGTCACACTGAA 42
||| ||| |||||||||||||||| | |||||||||||||||||||
Db 367 ATTGCCATCCACCAAGATGTCTGAACGTCAAGTCTTGCTAACCTCAGTCACACTGAA 42

421 ATATGGTACTTCTATATAGACAGAAAATCTGGCATCAATAATTGACCGTCGTCATCC 48
 427 ATAGTACCAATTCTCTAATATACAGAAA--TGCTACATAAATTGACCGTCGTCATCT 48

481 ATATCAAGGTATCCACAGAACCCCAAGGAGATGTAATTTTGGTAAATAACCGAGAAATTCAGT 54
|||||
484 ATACACGGTTACCCAGAACCTTAAGAAGATGAGTGTTTTGGTAAGAACCAAGAATTCACCT 54

D6
544 ATCAGTATGATGTATTATGCAGAATCTCAAGATAATGCACAGAACTGTACGACGTT 60

604 TCATCAGCTGTCTGTTTCATTTCCCTGATGTTACGAGCAATATGACCATTCTGTATT 66

Db 664 CTGCAACTGACACAGACGGCGCTTTATCTCACCCTTCTCTATAGA 710

RESULT 13				
AR159758				
LOCUS	1002 bp	DNA	linear	PAT 17-00
AR159758				

ACCESSION	AR159758
VERSION	AR159758.1
KEYWORDS	GI:16222530

ORGANISM	REFERENCE
Unknown.	1 (bases 1 to 1002)
Unclassified.	

TITLE	Antigen presenting system and methods for activation of T-cell
JOURNAL	Patent: US 6251627-A 33 26-JUN-2001;
FEATURES	Location/Qualifiers

	/organism="unknown"			
BASE COUNT	309 a	215 c	203 g	275 t
ORIGIN				

Query Match 55.2%; Score 463.8; DB 6; Length 1002;

Best Local Similarity	80.58;	Pred. No.	8.7e-113;
Matches	569;	Conservative	0;
		Mismatches	132;
		Indels	6;
		Gaps	2;

[illegible]

RESULT 11			
ARI60451			
LOCUS	ARI60451	751 bp	DNA
DEFINITION	Sequence 34 from patent US 6255073.		linear
			PAT 17-OCT-2001

Query match, 55.28; Score 463.8; DB 6; Length 751;

Best Local Similarity	80.5%;	Pred. No. 8.7e-113;
Matches	569;	Conservative 0;
	Mismatches 132;	Indels 6;
		Gaps 2;

OY	1	ATGTAATCTCGAGATGCACTATGAGAACTGAATAAATCTCTCTTGTGTGATGACCTCTCTGCTC	60
Db	7	ATGGAATCCCAAGTCACTATATGGGACTGATACATCTCTTGTGTGATGGCTTCTCTCCGCTC	66
OY	61	TATGTGCTGCTTTCATGAAAGAGTCAGAACGATATTTTCAACAAGCTGAGAACTGGCCATGC	120
Db	67	TCTGTGCTGCTCTCTCGAAGATTCAGAGCTTATTTTCAATAGACTCAAGACCTGGCCATGC	126
OY	121	CATTTCGCAATTTCTCAAAAATATAGCGCTGATGAGTGTGTACTGTTTTGGCGAGACAG	180
Db	127	CAATTTGCAAACTCTCAAAAACCAAGAGCTGAGTGAAGCTAGTACTATTTTGGCAGACAG	186
OY	181	GATTAAGCTGTTTGTACGAGCTATATCAGAGGCAAGAGAAACCTCAAAATGTTCAATCCG	240
Db	187	GA AAACTGTTCTGTAATGAGGTATCTTATGGCCAAAGAAATTTGCAAGTGTTCATCTC	246
OY	241	AAGTATTAAGGGCCGACAGAGTTTGGACAAGACATTTGGACCGCTGAGACCTCAATAATT	300
Db	247	AAGTATTAAGGGCCGACAGAGTTTGGACAGTTTGGATTCGACAGTTGGAACCTGAGACCTCAAAATCTT	306
OY	301	CAGATCAAGGACCAAGGGCTTGATCAATGTTTCTTATCATATAAAGGCCCAAGAGACTC	360
Db	307	CAGATCAAGGACCAAGGGCTTGATCAATGATATCATCATCAAAAAGCCCAAGAGATG	366
OY	361	GTTCCCATGAGCAACAGATAAATTGCACTATCACTGCTGCTTAATCTCACTCAACCTGAA	420
Db	367	ATTGCAATCCACAGATATAATTTCTGACTGCACTGCTGTTACTTCAGTCAAACTGAA	426
OY	421	ATAATGGTAACCTCTAATAGAAACAGAAAATTTCTGGCATCATAAATTGACCTGCTCATCC	480
Db	427	ATAGTACCAATTTCTAATATATTAACAGAAAA---TGTGTACATAAAATTTGACCTGCTCATCT	483
OY	481	ATACAGAGTTTCCCAAGAACCCAGAGAGATGATTTTGGATTAAGAAACCGAGAAATTCAGT	540
Db	484	ATATACAGGTTACCCAGAACTTATAGAAAGTATGAGTGTTTTGTATACAAACCAAGAAATTCACCT	543
OY	541	ACTAAGTATGATATCTGATGATGAAGAAATCTCAAAATAATATGTACAGAACTCTACACGTT	600
Db	544	ATCGAGTATGATGATATATATGAGAAATCTCAAGATATATGTACAGAACTGTACAGGTT	603
OY	601	TCTATACAGTTTCTCTTCTCACTGCTCCCTGAG---CAACGATATGAGAGATGTTCTGTGTC	655
Db	604	TCCATCAGCTTCTCTGTTTCATTTCCCTATGATGTATAGACAAATATGACCATCTTCTGTAATT	666
OY	658	CTTGCAACTTGATGCAATGAGATCTCCCTCCCATCTTAAATATAGA 704	
Db	664	CTTGCAACTTGATGCAAGAGCGGGCTTTTATCTTCACTTCTCTCATATAGA 710	

RESULT	12
ARI47736	
LOCUS	ARI47736 1002 bp DNA linear
DEFINITION	Sequence 33 from patent US 625042.
ACCESSION	ARI47736
VERSION	ARI47736.1 GI:15111826

Query Match 55.28; Score 463.8; DB 6; Length 1002;

Best Local Similarity 83.0%; Pred. No. 3.6e-118;
Matches 579; Conservative 0; Mismatches 110; Indels 9; Gaps 2;

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QY 19 ATGGAAGCAATATACATTCCTCTTTGTGATGACCTCCTGCTCATGTCGTCCTCCANG 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGAGCTAGTAACATTCCTCTTTGTGATGACCTCCTGCTCATGTCGTCCTCCANG 60

QY 79 AAGAGCAAGCAATATTCACACAAAGCTGAGAACTGCCATGCCATTTTACAAATTCGAA 138
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Db 61 AAAAGTCAGCAATATTCACAAAGCTGAGAACTGCCATGCCATTTTACAAATTCGAG 120

QY 139 AACATAGGCTGATGATGTTGGTAAGTGGCAGACAGATTAAGCTGTTCTGTAC 198
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Db 121 AACCTAAGCTGATGATGATGTTGGCAGACAGATTAAGCTGTTCTGTAC 180

QY 199 GAGCTATACAGAGCAAGAGAACCTCAAAATGTCATGCGAAGTAAAGGCGCCACA 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GAGCTATACAGAGCAAGAGAACCTCAAAATGTCATGCGAAGTAAAGGCGCCACA 240

QY 259 AGCTTTGACAAGCAATTTGACCTGAGACTCCATATATTCAGATCAAGAGCAAGGCG 318
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Db 241 AGCTTTGACAAGCAAGCAATTTGACCTGAGACTCCATATATTCAGATCAAGAGCAAGGCG 300

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QY 439 AGAAGCAAAATTTGCGCATCAAAATTTGACCTGCTCATCACTCACTCACTCACTCACT 498
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Db 421 CACACGAAATTTGCGCATCAAAATTTGACCTGCTCATCACTCACTCACTCACTCACTCACT 477

QY 499 CCCAAGGAGATGATTTTTTGTGTAAGCAAGCAATTCAGTACTAGTATGATGATGATG 558
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Db 478 CCCAAGGAGATGATTTTTTGTGTAAGCAAGCAATTCAGTACTAGTATGATGATGATG 537

QY 559 ATGAAGAATCTCAAAATATGTCACAGACTGACAACTGTTCTGATGATGATGATGATG 618
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Db 538 ATGAAGAATCTCAAAATATGTCACAGACTGACAACTGTTCTGATGATGATGATGATG 597

QY 619 TCAGTCCGTCGAGCAAGCAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
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Db 598 CCATCCCTCCGAGCAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 657

QY 678 -----GCTTCCTCCCTACTTATATATAGAAACCA 710
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Db 658 ACACCTCTTCTCTCTACTTATATATAGATGAA 695
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RESULT 9

ARI47737

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

55.2%; Score 463.8; DB 6; Length 751;

Best Local Similarity 80.5%; Pred. No. 8.7e-113;
Matches 569; Conservative 0; Mismatches 132; Indels 6; Gaps 2;

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QY 1 ATGATCTCAGATGACACTATGGAAGTAAATACATTCCTTTGTGATGACCTCCTCCTC 60
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Db 7 ATGATCTCAGATGACACTATGGAAGTAAATACATTCCTTTGTGATGACCTCCTCCTC 66

QY 61 TATGCTCTCTCTCCATGAGAGTCAAGCATATTTCAACAGACTGAGAGACTGCCATGC 120
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Db 67 TCTGCTCTCTCTCTCCATGAGAGTCAAGCATATTTCAACAGACTGAGAGACTGCCATGC 126

QY 121 CATTTCAAAATTCCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATGATG 180
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Db 127 CAATTTCAAAATTCCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATGATG 186

QY 181 GATAGCTGTTCTGTACAGACTATACAGAGCAAGAGAACCCCAAAATGTTCAATGC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 GAAAACTGTTCTGTACAGACTATACAGAGCAAGAGAACCCCAAAATGTTCAATGC 246

QY 241 AAGTATAGAGGCGCCACAGCTTTCACAAAGCAATTTGACCTGAGACTCCATATATTT 300
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Db 247 AAGTATAGAGGCGCCACAGCTTTCATTTGATTTGAGACAGTTGAGACCTTACAAATCTT 306

QY 301 CAGATCAAGCAAGGCTTTGATCAATGTTGTTCAATCATATTAAGGCCCAAGGACTC 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 307 CAGATCAAGCAAGGCTTTGATCAATGTTGTTCAATCATATTAAGGCCCAAGGACTC 366

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Db 367 ATTGCTATCCACAGATGATTTGCTGACATGACGCTGCTGCTGCTGCTGCTGCTGCTG 426

QY 421 ATAATGTAACCTTCTAATAGAACGAAATTTGCTGCATCATTAATTTGACTGCTCATCC 480
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Db 427 ATATGTAACCTTCTAATAGAACGAAATTTGCTGCATCATTAATTTGACTGCTCATCT 483

QY 481 ATCAAGGTTACCCAGACCAAGGAGATGATTTTTTGTGTAAGCAAGCAATTCAGT 540
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QY 601 TCTATGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
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Db 604 TCTATGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663

QY 658 CTGCACTTGAAGTCAATGAAGCTTCCCTCCCTCACTTATATATAG 704
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RESULT 10

ARI59759

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

55.2%; Score 463.8; DB 6; Length 751;

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LOCUS PIGCD86G 994 bp mRNA linear MAN 17-JUN-1997
DEFINITION Sus scrofa CD86 mRNA, complete cds.
ACCESSION L76099.1 GI:2198558
VERSION L76099.1 GI:2198558
KEYWORDS T cell costimulation.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 994)
Bohner, S.E., Karmann, K., Min, W., Hughes, C.C., Pober, J.S. and
Bohner, A.L.
Porcine endothelial CD86 is a major costimulator of xenogeneic
human T cells: cloning, sequencing, and functional expression in
human endothelial cells
JOURNAL J. Immunol. 157 (9), 3838-3844 (1996)
MEDLINE 97047772
COMMENT GSDB:S:74002
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KTLFLSPCNIDAKPVQPDHILWIAALVIVVCGVSVFLIRKKRKKQGPS
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BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN
Query Match 57.6%; Score 484; DB 4; Length 994;
Best local Similarity 83.0%; Pred. No. 3,6e-118;
Matches 579; Conservative 0; Mismatches 110; Indels 9; Gaps 2;
Qy 19 ATGGAAGTCAATATCTCTTTGATGACCCCTGCTCTATGAGTCTGCTTCATG 78

Db 1 ATGGAAGTCAATATCTCTTTGATGACCCCTGCTCTATGAGTCTGCTTCATG 60
Qy 79 AAGAGTCAAGCATATTTCAACAGAGCTGAGAACTGCCATGCCATTTTACAAATTC 138
Db 61 AAAAGTCAAGCATATTTCAACAGAGCTGAGAACTGCCATGCCATTTTACAAATTC 120
Qy 139 AAGCATAGAGTGGATGAGTGGTGTAGTGTGTTGGCAGCAGCAAGTAAGCTGCTG 198
Db 121 AACCTAGAGCTGGATGAGTGGTGTAGTGTGTTGGCAGCAGCAAGTAAGCTGCTG 180
Qy 199 GAGCTATACAGAGCAAGAGAGACCTCAAAATGTTCAATGCCAAGTATAGGCCGCA 258
Db 181 GAGCTATACAGAGCAAGAGAGACCTCAAAATGTTCAATGCCAAGTATAGGCCGCA 240
Qy 259 AGCTTGGACCAAGCAATTTGACCCCTGAGACCTCCATATATGATGATAGAGAGG 318
Db 241 AGCTTGGACCAAGCAATTTGACCCCTGAGACCTCCATATATGATGATAGAGAGG 300
Qy 319 TTTGATCAATGTTTGTTCATCATATTAAGGCGCCAAAGGACTGTTCCATGACCAATG 378
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Qy 379 AATTCGACCTATGAGTGTCTTCTACTTCACTTCACTGAACTGAAATATAGTACTCT 438
Db 361 AGTTCTGACCTATGATGTTGCTTCTTCACTTCACTGAACTGAAATATAGTACTCT 420
Qy 439 AGAAGCAAAATTTGCGATCATTAATTTGACCTGCTCATCCATCAAGGTTACCCAG 498
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Qy 499 CCCAAGAGATGATTTTGTGTAAGACCGAGATTTCAAGTCAAGTATGATGATG 558
Db 478 CCCAAGAGATGATTTTGTGTAAGACCGAGATTTCAAGTCAAGTATGATGATG 537
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Db 538 ATGAAGAAATTCATAATATGATGATGATGATGATGATGATGATGATGATGATG 597
Qy 619 TCAATCCCTGAGAGCAAGATGAGCATCTTCTGCTGCTGCACTTATGATGATG 677
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Qy 678 -----GCTTCCCTCCCTACTTATATATAGAAACCA 710
Db 658 ACACTGCTTTTCTCCCTACTTATATATAGATGACAA 695

RESULT 8
AX027016 994 bp DNA linear PAT 16-SEP-2000
LOCUS AX027016
DEFINITION Sequence 13 from Patent WO0037102.
ACCESSION AX027016
VERSION AX027016.1 GI:10188045
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 994)
Rogers, N.J., Dorling, A. and Lechler, R.I.
Immunosuppression
Patent: WO 0037102-A 13 29-JUN-2000;
ROGERS, NICHOLA JANE (GB) ; DORLING, ANTHONY (GB) ;
LECHLER, ROBERT IAN (GB)
TITLE
LECHLER ROBERT IAN (GB)
FEATURES
location/Qualifiers
source 1..994
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN
Query Match 57.6%; Score 484; DB 6; Length 994;

Best Local Similarity 89.4%, Pred. No. 2.4e-144;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

14 GCACATGGAAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCTT 73
195 GCACATGGAAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCTT 254

74 CCATGGAAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCTT 133
255 CCATGGAAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCTT 314

134 CTCGAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 193
315 CTCGAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 374

194 TGTAGAGCTATACAGAGGCAAGAACCTCCAAATGTTCTGCACTATTAAGGCC 253
375 TGTAGAGCTATACAGAGGCAAGAACCTCCAAATGTTCTGCACTATTAAGGCC 434

254 GCACAGCTTTGACAAAGCAATTTGACCTGAGACTCATATATTCAGATCAAGACA 313
435 GTCAAGCTTTGACAAAGCAATTTGACCTGAGACTCATATATTCAGATCAAGACA 494

314 AGGGCTTGTATCAATGTTTCTGTCATCAATAAGGCCCCAAAGAGCTGTTCCATGAC 373
495 AGGGCTTGTATCAATGTTTCTGTCATCAATAAGGCCCCAAAGAGCTGTTCCATGAC 554

374 AGATGAATTCGACCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
555 AATGAGCTTGTACCTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614

434 CTATATGAACAGAAATTCCTGATCATTAATTTGACCTGCTCATCAATCAAGGTTAC 493
615 CTATATGAACAGAAATTCCTGATCATTAATTTGACCTGCTCATCAATCAAGGTTAC 674

494 CAGAACCCAGAGAGATGTTTGTGTAAGAACGAGAAATTCAGATCAAGATGATGAT 553
675 CAGAACCCAGAGAGATGTTTGTGTAAGAACGAGAAATTCAGATCAAGATGATGAT 734

554 CTGTCAATGAAGAAATTCCTGATCATTAATTTGACCTGCTCATCAATCAAGGTTAC 613
735 CTGTCAATGAAGAAATTCCTGATCATTAATTTGACCTGCTCATCAATCAAGGTTAC 794

614 CCTTTCAGTCCCTGAGAGCAATGATGATGATGATGATGATGATGATGATGATGAT 673
795 CTTTTCAGTCCCTGAGAGCAATGATGATGATGATGATGATGATGATGATGATGAT 854

674 T---GAAGCTTCCCTGCTACCTTATTAATATGAAACCAACAAAGTGAGAGAAA 725
855 TGGAGATGCTGCTCCCTACCTTATTAATATGAAACCAACAAAGTGAGAGAAA 909

RESULT 6
AF344836 901 bp mRNA linear PRI 06-SEP-2001
LOCUS AF344836
DEFINITION Papio cynocephalus anubis CD86 protein precursor, mRNA, complete cds.
ACCESSION AF344836
VERSION AF344836.1 GI:13649983
KEYWORDS
SOURCE
ORGANISM
Olive baboon.
Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE
AUTHORS Villinger, F., Bostlik, P., Mayne, A.E., King, C.L., Genain, C.P.,
Weiss, W.R. and Ansari, A.A.
TITLE Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules
JOURNAL Immunogenetics 53 (4), 315-328 (2001)
MEDLINE 2138318
PUBMED 11491535

REFERENCE 2 (bases 1 to 901)
AUTHORS Villinger, F.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2001) Pathology and Laboratory Medicine, Emory
University School of Medicine, Winship Cancer Institute, 1365B
Clifton Rd. Atlanta, GA 30322, USA
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sig_peptide
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/note="87.2"
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SELVFWQMOENLVLENYLIGREKFDVSHKVMGRSFDESWTLRLHLQITDKGLY
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FMSVLRTRKNTTEYDGMOKSODNTELYDVISISVSFPPVTSNMNITFCVLETDK
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630
misc.feature
/note="144 nucleotide insertion in Homo sapiens CD86"
BASE COUNT 281 a 193 c 178 g 249 t
ORIGIN
Query Match 62.0%; Score 520.4; DB 9; Length 901;
Best Local Similarity 79.0%; Pred. No. 7.3e-128;
Matches 659; Conservative 0; Mismatches 166; Indels 9; Gaps 3;

13 TGCATATGGAAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCT 72
1 TGCATATGGAAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCT 60

73 TGCATGAGAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCT 132
61 CCCCTGAGAGTGAATACATTCCTCTTGTGATGACCTCCCTCTGATGCTGCT 120

133 TCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 192
121 TCTCAAAACATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 180

193 CTGTAGAGCTATACAGAGGCAAGAACCTCCAAATGTTCTGATCAATCAAGGTTAC 252
181 CTGTAGAGCTATACAGAGGCAAGAACCTCCAAATGTTCTGATCAATCAAGGTTAC 240

253 CGCACAAGCTTTGACAGCAAGCAATTTGACAGCTGATCAATATTAATCAAGAGAC 312
241 CGCACAAGCTTTGACAGCAAGCAATTTGACAGCTGATCAATATTAATCAAGAGAC 300

313 AAGGGCTTGTATCAATGTTTCTGTCATCAATTAAGGCCCCAAAGAGCTGTTCCATGAC 372
301 AAGGGCTTGTATCAATGTTTCTGTCATCAATTAAGGCCCCAAAGAGCTGTTCCATGAC 360

373 CAGATGAATTCGACCTATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
361 CAGATGAATTCGACCTATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

433 TCTATATGAACAGAAATTCCTGATCATTAATTTGACCTGCTCATCAATCAAGGTTAC 492
421 TCTATATGAACAGAAATTCCTGATCATTAATTTGACCTGCTCATCAATCAAGGTTAC 477

493 CCAGAACCCAGAGAGATGTTTGTGTAAGAACCGAAGATTCAGATCAATCAATGAT 552
478 CCAGAACCCAGAGAGATGTTTGTGTAAGAACCGAAGATTCAGATCAATCAATGAT 537

553 ACTGTCAAGAGAAATTCCTCAAAATATGTCACAGAGCTTCACAGCTTTCATCAGCTTG 612
538 GGTGTATGAGAAATTCCTCAAAATATGTCACAGAGCTTCACAGCTTTCATCAGCTTG 597

613 TCTTTCATGCTCCCTGAG---CAAGCAATGTGACACATCTTGTGTGCTGCTCAACTGAG 669

[illegible]

Db	Accession	Gene	Protein	Length	Score	DB	Length
Db	556	AGGCGACATATCACTGTTTTCATTATATAAAGGCGCCAAAGACATGTTCCCATGCACC	615				
Qy	374	AGATGAAATTCGACCTATCACTGCTTGTCTTAACCTCAAGTCAACCTGAATAATGTAAGT	433				
Db	616	AAATGAGTTTGTGACCTATCACTGCTTGTCTTAACCTCAAGTCAACCTGAATAATGTAAGT	675				
Qy	434	CTAATGAAAGAAATCTGACATCAATAATTTGACCTCTCATCCATCAAGAGTTACC	493				
Db	676	CTAATGAAAGAAATCTGACATCAATAATTTGACCTCTCATCCATCAAGAGTTACC	735				
Qy	494	CAGAACCCAGAGAGATGTAATTTTTTGGTAAAAACCGAGAAATTCAGTACGTAAGTATATA	553				
Db	736	CAGAACCCAGAGAGATGTAATTTTTTGGTAAAAACCGAGAAATTCAGTACGTAAGTATATA	795				
Qy	554	CTGTATGTAAGAAATCTCAAAATATATGTCACAGAACTCTACACAGTTTCATCAGTTGT	613				
Db	796	CTGTATGTAAGAAATCTCAAAATATATGTCACAGAACTCTACACAGTTTCATCAGTTGT	855				
Qy	614	CTTCTCAGTCCCTGAGCAAGCAATGTGAGCACTCTTGTGTCTCTGCATCTTAAGTCA	673				
Db	856	CTTCTCAGTCCCTGAGCAAGCAATGTGAGCACTCTTGTGTCTCTGCATCTTAAGTCA	915				
Qy	674	T---GAGAGTTCCCTCCCTACCTTATATATGAAACCAACCAAGTGTGAGAGAA	725				
Db	916	TGAGATGTGCTGCTCTCCCTACCTTATATATGAAACCAACCAAGTGTGAGAGAA	970				
RESULT 5	AY007704	2830 bp	mRNA	Linear	MAM 03-OCT-2001		
LOCUS	AY007704	Felis catus CD86 (CD86) mRNA, complete cds.					
DEFINITION	AY007704						
VERSION	AY007704.1	GI:15418725					
KEYWORDS							
SOURCE		cat.					
ORGANISM		Felis catus					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS		Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.					
TITLE		1 (bases 1 to 2830)					
JOURNAL		Yang, S., Sellins, K.S., Powell, T., Stoneman, E. and Sim, G.K.					
MEDLINE		Costimulatory molecules					
PubMed		vet. Immunol. Immunopathol. 81 (1-2), 15-21 (2001)					
REFERENCE		2 (bases 1 to 2830)					
AUTHORS		Yang, S.					
TITLE		Direct Submission					
JOURNAL		Submitted (06-SEP-2000) Immunology, Heskia Corporation, 1613					
FEATURES		Prospect Parkway, Ft Collins, CO 80525, USA					
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		SLDQGYHCFLYHKGKRGSLPMHQSLSLVSANYSOPELIVTSKRITNSGILNTCS					
		SLDQYEPKEMFQLTENSTTKYDLYVMKSSQNTVLELYNSLSLPSVPEAHNVSV					
		CALEKTELMELSLPNTIDACPDKDPEGHMLAAVLVMEVVCQGVSRKTLKKR					
		KKQPGSHCEETIKRKRKSKOTNEVRYPHVERSDAQCINILKTASGDSTHF"					
BASE COUNT		877 a 570 c 586 g 797 t					
ORIGIN							
Query Match		69.3%; Score 582.2; DB 4; Length 2830;					


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Db 66 TATGTCGTCTCCATCATGAGAGTCAACATATTTCAACAGACTGAGAAAGTCCATGC 125
QY 121 CATTTACAAATTTCTCAAAACATAGCCGTGATGCTGTGATGTTGGCAGGACCA 180
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QY 181 GATAGCTGGTCTGTACAGCTATACAGAGCAAGAAACCTCAAAATGTTTCATGC 240
Db 186 GATAGCTGGTCTGTACAGCTATACAGAGCAAGAAACCTCAAAATGTTTCATGC 245
QY 241 AATATAAGGGCCGACAAAGCTTTGACAAAGACAAATTTGACCCGACATCCATATAT 300
Db 246 AAGTATAGGGCCGACAAAGCTTTGACAAAGACAAATTTGACCCGACATCCATATAT 305
QY 301 CAGATCAAGAGACAGAGGCTTGTATCATGTTTCATCATATTAAGGCGCCAAAGACTC 360
Db 306 CAGATCAAGAGACAGAGGCTTGTATCATGTTTCATCATATTAAGGCGCCAAAGACTC 365
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Db 366 GTTCCATGACACAGATGATGATCTGACCTATCAGTGGCTGTACTTCACTCAACCTGAA 425
QY 421 ATAATGTAACTTCTAATAGAACAGAAATTCGTGCATCATMAATTTGACCTGCTATCC 480
Db 426 ATAATGTAACTTCTAATAGAACAGAAATTCGTGCATCATMAATTTGACCTGCTATCC 485
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Db 546 ACTAAGTATGATGATGTCATGTAAGAAATCTCAAAATAATGTACAGAACTCTCAAGTT 605
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Db 606 TCTATAGCTTGTCTCTCATAGTCCCTGAGCAAGCAATGAGCACTCTCTGTCTG 665
QY 661 CAACCTGAGTCAATGAAAGCTTCCCTACCTTATATATATAGAACCAACA 712
Db 666 CAACCTGAGTCAATGAAAGCTTCCCTACCTTATATATATAGATGACATA 717

RESULT 3
AF157827 1138 bp mRNA linear MAM 08-MAY-2000
LOCUS AF157827
DEFINITION Fells catus CD86 antigen (CD86) mRNA, complete cds.
ACCESSION AF157827
VERSION AF157827.1 GI:5381423
KEYWORDS
SOURCE
cat.
Fells catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
REFERENCE
1 (bases 1 to 1138)
Choi, I.-S., Hash, S.M., Winslow, B.J. and Collisson, E.W.
Sequence analyses of feline B7 costimulatory molecules
JOURNAL Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)
MEDLINE 20180222
PUBMED 10713336
REFERENCE
2 (bases 1 to 1138)
Choi, I.-S., Hash, S.M., Winslow, B.J. and Collisson, E.W.
Direct Submission
JOURNAL Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M
University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA
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63..1052
CDS
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STOGYDEPEKEMFOLNTENSTTKYKDYMKRSONNVTELYVNSISLPEPSVEAHNVSVF
CALKLETEMLSLPENIDAOBKDKDEPOGHFLIAVLVMPFVPGMVSFKTLRRK
KKQPGSHCEETIKERKESKQTERNPYHNPERSDEADCCVNILKTSADKNG"
BASE COUNT 358 a 243 c 246 g 289 t
ORIGIN
Query Match 69.3%; Score 582.2; DB 4; Length 1138;
Best Local Similarity 89.4%; Pred. No. 2,5e-144;
Matches 639; Conservative 0; Mismatches 73; Indels 3; Caps 1;
QY 14 GCATATGSAAGCATTAATCATCTCTGTGATGATGACCTCCTGCTCATGCTGCTGCT 73
Db 79 GCATATGSAAGCATGAGCACACTCTCTGTGATGATGACCTCCTGCTCATGCTGCTGCT 138
QY 74 CCATGAGAGTCAAGCATATTTTCACAGACATGAGAACTGCATGCTTTTCAAAAT 133
Db 139 CCATGAGAGTCAAGCATATTTTCACAGACATGAGAACTGCATGCTTTTCAAAAT 198
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Db 319 GTACAACTTTGACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 378
QY 314 AGGCTTGTATCATGATGTTTGGTTCATCATTAAGGGCCCAAGAGCTGTCATGACCC 373
Db 379 AGGCTTGTATCATGATGTTTGGTTCATCATTAAGGGCCCAAGAGCTGTCATGACCC 438
QY 374 AGATGATTTCTGACCTATGAGTCTGCTGATGATGATGATGATGATGATGATGAT 433
Db 439 AATGATTTCTGACCTATGAGTCTGCTGATGATGATGATGATGATGATGATGATGAT 498
QY 434 CTATATAGACAGAAATTTGAGCATTAATTTGACCTGCTCATCATCATCATCATCAT 493
Db 499 CTATATAGACAGAAATTTGAGCATTAATTTGAGCATTAATTTGAGCATTAATTTGAG 558
QY 494 CAGAACCCAGAGATGATTTTGTGTAAGAACCGAAGATTCATGATGATGATGATGAT 553
Db 559 CAGAACCCAGAGATGATTTTGTGTAAGAACCGAAGATTCATGATGATGATGATGAT 618
QY 554 CTGTCATGAGAAATTCACAAATATGATGATGATGATGATGATGATGATGATGATGAT 613
Db 619 CTGTCATGAGAAATTCACAAATATGATGATGATGATGATGATGATGATGATGATGAT 678
QY 614 CTTTCTAGTCCCTGAGACAGCATGATGATGATGATGATGATGATGATGATGATGAT 673
Db 679 CTTTCTAGTCCCTGAGACAGCATGATGATGATGATGATGATGATGATGATGATGAT 738
QY 674 T---GAAGCTTCCCTGACCTTATATATGATGATGATGATGATGATGATGATGAT 725
Db 739 TGGAGATGCTGCTCTCCCTTACCTTTCAATATGATGATGATGATGATGATGATGAT 793

RESULT 4
AB030652 1270 bp mRNA linear MAM 01-MAR-2001
LOCUS AB030652
DEFINITION Fells catus mRNA for B-lymphocyte activation antigen B7-2 (CD86),
complete cds.
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Best Local Similarity 100.0%; Pred. No. 5.8e-213;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 7 ATGTATCTCAGATGACATGTAATGACATGTCCTCTTGTGATGACCTCTCTCTC 66
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DB 67 TATGGTCTGCTTCCATGACAGATGATATTTCAACAAGACTGGAGAAGTCCATGC 126
OY 121 CATTTTCAAAATTCACAAACATGAGCTGATGAGTTGGAGTGTGTTGGCAGACAG 180
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DB 127 CATTTTCAAAATTCACAAACATGAGCTGATGAGTTGGAGTGTGTTGGCAGACAG 186
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DB 187 GATAAGCTGTTCTGTACAGCTATACAGAGCAAGAAAGAAAGAACTCTCAAAATGTTCAATGC 246
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DB 247 AAGTATAAGGGCCGACAGAGCTTTGACAAAGCAATTTGACCTGAGACTCCATATATT 306
OY 301 CAGATCAAGAGCAAGGCTTGTATCAATGTTTCTTCATCAATAAAGGCCCAAGGACTC 360
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DB 307 CAGATCAAGAGCAAGGCTTGTATCAATGTTTCTTCATCAATAAAGGCCCAAGGACTC 366
OY 361 GTTCCATGACACAGATGATTTCTGACCTATCAGTGTGCTTACTTACTGCAACCTCAA 420
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DB 607 TCTATCAGCTTGTCCTTCTCAGTCCCTGAAAGCAAGCAATGTGACATCTTGTGCTCG 666
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DB 667 CACTTGAAGTCAATGACACTTCCCTCCCTACTTATATATAGAAACCAACAAAGTGAG 726
OY 721 AGAAAGAAAGTGAACACACACAGCAAGAAAGTACGATACATGAAGGAAATCTGAT 780
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DB 727 AGAAAGAAAGTGAACACACACAGCAAGAAAGTACGATACATGAAGGAAATCTGAT 786
OY 781 GAGCCAGAGTGTGTTTACATTTTCAAGACAGCTTCAGGCGACACACAGTACACAGTT 840
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DB 787 GAGCCAGAGTGTGTTTACATTTTCAAGACAGCTTCAGGCGACACACAGTACACAGTT 846

RESULT 2
LOCUS      AF106826      1897 bp      mRNA      linear      MAM 14-DEC-1999
DEFINITION Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
ACCESSION AF106826
VERSION    AF106826.1 GI:6572516
KEYWORDS
SOURCE     dog.
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 1897)
            Yang,S. and Sim,G.-K.
            New forms of dog CD80 and CD86 transcripts that encode secreted B7
            molecules
            Immunogenetics 50 (5-6), 349-353 (1999)
JOURNAL   2 (bases 1 to 1897)
            Yang,S. and Sim,G.-K.
            Direct Submission
            Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
            Sharp Point Drive, Fort Collins, CO 80525, USA
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Best Local Similarity 99.3%; Pred. No. 9.3e-177;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 6 ATGTATCTCAGATGACATGTAATGACATGTCCTCTTGTGATGACCTCTCTCTC 65
OY 61 TATGGTCTGCTTCCATGACAGATGATATTTCAACAAGACTGGAGAAGTCCATGC 120
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 1150.19 Seconds
(without alignments)
15282.914 Million cell updates/sec

Title: US-09-646-561-19

Perfect score: 840
Sequence: 1 atgtatctcagatgcactat.....acacagctactacacagttt 840

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inh:*
32: em_hlg_other:*
33: em_hlg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	length	DB	ID	Description
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1	840	100.0	1795	4	AF106827	Canis fam
2	704	83.8	1897	4	AF106826	Canis fam
3	582.2	69.3	1138	4	AF157827	Felis cat
4	582.2	69.3	1270	4	AB030652	Felis cat
5	582.2	69.3	2830	4	AY007704	Felis cat
6	520.4	62.0	901	4	AF344836	Papio cyn
7	484	57.6	994	4	PICGD865	Sus scrofa
8	484	57.6	751	6	AX027016	Sequence
9	463.8	55.2	751	6	AR147737	Sequence
10	463.8	55.2	751	6	AR159759	Sequence
11	463.8	55.2	751	6	AR160451	Sequence
12	463.8	55.2	1002	6	AR147736	Sequence
13	463.8	55.2	1002	6	AR159758	Sequence
14	463.8	55.2	1002	6	AR160450	Sequence
15	463.8	55.2	1112	6	HDM872A	Sequence
16	463.8	55.2	1120	6	AR030780	Sequence
17	463.8	55.2	1120	6	AR112747	Sequence
18	463.8	55.2	1120	6	AR146413	Sequence
19	463.8	55.2	1120	6	AX047043	Sequence
20	463.8	55.2	1161	6	AR146414	Sequence
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22	458.8	54.6	1424	6	AX332506	Sequence
23	458.8	54.6	1424	9	HSU04343	Sequence
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25	453.8	54.0	738	6	AX002781	Sequence
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30	447.6	53.3	1044	9	AF344851	Sequence
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44	339.6	40.4	2528	10	BC013807	Mus muscu
45	337.2	40.1	1261	6	AR146408	Sequence

ALIGNMENTS

RESULT 1
AF106827
LOCUS
DEFINITION Canis familiaris truncated B7-2 protein (CD86) mRNA, complete cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1795)
Yang, S. and Sim, G.-K.
TITLE
New forms of dog CD80 and CD86 transcripts that encode secreted B7
molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20093996
REFERENCE 2 (bases 1 to 1795)
Yang, S. and Sim, G.-K.
TITLE Direct Submission
Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825
Sharp Point Drive, Fort Collins, CO 80525, USA
FEATURES
Location/Qualifiers

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Db 1034 ATATACCTGAAAGTCTGATGAAGCCGCGTGTGTTTAAAGTTCGAAGACATCTTCAT 1093
QY 965 GCGACAACAGTACTACACAGTTT 987
Db 1094 GCGACAAGAGTGATACATGTTT 1116
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Search completed: October 19, 2002, 23:35:40
Job time : 45.2281 secs

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Qy 181 GATTAAGCTGGTCTCTAGCAGCTATACAGAGGCAAGAACCTCAAAATGTTCATGCC 240
Dh 328 GAAAACCTTGTTCTGATGAGGTATACCTTAGCAAAAGAAATTTGACAGTCTTATTC 387
Qy 241 AAGTAAAGGGCCGACAAAGCTTTGCAAAAGCAATTTGGACCTTAGACTCCATATAT 300
Dh 388 AAGTAAATGAGGCGCCGCAAGGTTTATTCGACAGTGTGACCTTAGACTCCATATCT 447
Qy 301 CAGATCAAGCAAGAGGCTTTGATCAATGTTTCTGTTCAATCAAGGCGCCCAAGAGCTC 360
Dh 448 CAGATCAAGCAAGAGGCTTTGATCAATGTTTCTGTTCAATCAAGGCGCCCAAGAGCTC 507
Qy 361 GTTCCCATGACCAAGATGATTTCTGACCTATGCTTGTCTGTAAGTCAAGCTGAA 420
Dh 508 ATTCCATCTCCACAGATGAAATCTGACCTGACGCTGCTGCTAAGTCAAGCTGAA 567
Qy 421 ATTAATGTAACCTTCTAATAGAACAAATTTGCGATCATTAATTTGACCTGCTCATCC 480
Dh 568 ATAGTACCAATTTCTAATATTAACAGAAAA--TGTTGATCAATAATTTGACCTGCTCATCT 624
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Dh 625 ATACAGGTTACCCAGAACCCAGAGATGATGTTTGTGTAAGAACCAAGATTTCAAGT 684
Qy 541 ACTAGTATGATCTGATGATGAAATCTCAAAATTAATGTCACAGAACTCTACAGCTT 600
Dh 685 ATCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
Qy 601 TCTATCAGCTTGTCTCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 657
Dh 745 TCCATCAGCTTGTCTCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 804
Qy 658 CTGCAACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 717
Dh 805 CTGCAACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861
Qy 718 CCCAGCCCTGATGAGAACCAATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 777
Dh 862 CCTAGGCTCCCCAGACCAATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 918
Qy 778 TTGTTGTGGAGTGTCTCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 834
Dh 919 ATATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 978
Qy 835 CCCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 894
Dh 979 AACCTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1038
Qy 895 AGAGTACGCTACATGAAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 951
Dh 1039 AGAGTACGCTACATGAAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1098
Qy 952 AAGCAGACTTCAGGCGCAACAGTACTACACAGTTT 987
Dh 1099 AAGCAGACTTCAGGCGCAACAGTACTACATGTTTT 1134

RESULT 15

US-09-326-186B-226
; Sequence 226, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326.186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31

NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 226
LENGTH: 1424
TYPE: DNA
ORGANISM: Homo sapien
US-09-326-186B-226

Query Match 57.8%; Score 570.2; DB 4; Length 1424;
Best Local Similarity 78.0%; Pred. No. 6,3e-164;
Matches 767; Conservative 0; Mismatches 198; Indels 18; Gaps 6;
Qy 14 GCATATGAACTGAATACATTTCTTTGATGACCTCCGCTGATAGTGGCTT 73
Dh 143 GCATATGAGGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 202
Qy 74 CCATGAAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGCTATTTTCAAAAT 133
Dh 203 CTCTGAAGATTCAGGCTTATTTCAATGAGACTGACAGCTGCCATGCTATTTTCAAACT 262
Qy 134 CTCAAAACATAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 193
Dh 263 CTCAAAACCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 322
Qy 194 TGTAGAGCTATACAGAGGCAAGAGAACCTCAAAATGTTCTATGCAAGTATTAAGGGCC 253
Dh 323 TGATAGGATATCTTAGGCAAGAGAAATTTGACAGTGTTCATTTCCAGTATATGGGCC 382
Qy 254 GCACAAAGCTTTGCAAAAGCAATTTGACCTGAGCTCCATTAATATTCAGATCAAGGACA 313
Dh 383 GCACAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 442
Qy 314 AGGCGTTGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 373
Dh 443 AGGCGTTGTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 502
Qy 374 AGATGATTTCTGACCTATACAGTGTGCTGATGATGATGATGATGATGATGATGATGATG 433
Dh 503 AGATGATTTCTGACCTATACAGTGTGCTGATGATGATGATGATGATGATGATGATGATG 562
Qy 434 CTATATGAGCAGAAATTTCTGSCATCATTAATTTGACCTGCTCATCATCATCATCATCAT 493
Dh 563 CTATATTAACAGAAA--TGTTGATCATTAATTTGACCTGCTCATCATCATCATCATCAT 619
Qy 494 CAGAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 553
Dh 620 CAGAACCTTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 679
Qy 554 CTGTCATGAAAGAAATCTGAAAATTAATGATGACAGAACTGACAGCTTCTATCAGCTTGT 613
Dh 680 GTATTATGCAAAATCTCAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 739
Qy 614 CCTTCAGTCCCTGAG--CAAGCAATGTGAGCATCTTCTGCTGCAACTTGTAGT 670
Dh 740 CTGTTTCATTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 799
Qy 671 CAATGAAGTTCCTTCCTACTTATTAATATGATGACATACGAACCAACCCCTGATG 730
Dh 800 AGACGCGCTTTATCTTCACTTCTCTATAGA--CGTTGAGAGCCCTGACGCTCC 856
Qy 731 GAGACCAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 790
Dh 857 CAGACCAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 913
Qy 791 TGTCTTTCTAACAATAAGAAA--AGAGAGAAAGACAGCTGGCCCTCTCATGAAT 847
Dh 914 TTTCTGCTATTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 973
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Dh 974 GTGGAACCAACCAATGAG 1033
Qy 908 ATGAAGCGAAAGATCTGATGAGAGCCAGTGT--TTAACAATTTGCAAGACAGCTTCAG 964

Db 821 CCTCAGCCTCCCCAGCACCACATCTCTTGATTAACAGCTGTACTTCCAA---CAGTATT 877
 QY 778 TTGTGGGATGGTGTCTTTCTTACACTAAGAAA---AGGAAGAAGACGACCTGGC 834
 Db 878 ATATGTGTGATGGTTTCTGTCTAATCTCTATGMAATGMAAAGAAAGAACGCGCTCGC 937
 QY 835 CCCCTCATGATGTGAACCAACAAAGTGAAGAAAGAAAGTGAAGACGACCAAGAA 894
 Db 938 AACCTTATATATGTGGAAACCAACACATGAGAGAGAGATGAACGACCAAGAA 997
 QY 895 AGAGTAGGACATGATAAGAGATCTGATGAAGCCAGTGTG---TTAACAATTTCG 951
 Db 998 AGAAGAAAATCCATATACCTGAAGATCTGATGAAGCCAGCGGTGTTTTAAAGTTCG 1057
 QY 952 AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
 Db 1058 AAGACATCTTCATGCGACAAAAGTGATACATGTTTT 1093

RESULT 11
 PCT-US95-02576-22
 ; Sequence 22, Application PC/TUS9502576
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
 ; TITLE OF INVENTION: and Uses Therefor
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/02576
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/205,697
 ; FILING DATE: 02-Mar-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: BWI-120CPPC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1120 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 107..1093
 ; PCT-US95-02576-22

Query Match 58.3%; Score 575.2; DB 5; Length 1120;
 Best Local Similarity 77.8%; Pred. No. 1,7e-165;
 Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

QY 1 ATGATATCAAGATGCATATGSAACATATCTCTTTGTGATGACCTCTGCTGC 60
 Db 107 ATGATATCAAGATGCATATGSAACATATCTCTTTGTGATGACCTCTGCTGC 166

QY 61 TATGGTGTGCTTCCATGATGAGATCAAGCATATTTCAACAGACTGAGAACCTCCATGC 120
 Db 167 TCTGGTGTGCTTCCATGATGAGATCAAGCATATTTCAACAGACTGAGAACCTCCATGC 226
 QY 121 CATTTTAAATAATTTCTAAATAAGTGAAGCTGGATGAGTGTGATGTTGGCAGGACCC 180
 Db 227 CAATTTGCAAACTCTCAAAACCAAGCCTGAGTGTGATGATTTTGGCAGGACCC 286
 QY 181 GATAAGCTGTCTCTAGAGAGTATACAGAGCAAGAAAGAAAGCCCAAAATGTCTATGC 240
 Db 287 GAAACCTGTGTTCTAAATGAGTATCTTAGGCAAGAGAAATTTGACAGTGTCTATCC 346
 QY 241 AAGTATTAAGGCGCCGACAAAGCTTTGACAAAGCAATTTGACCTGAGACTCCATATATT 300
 Db 347 AAGTATTAAGGCGCCGACAAAGCTTTGACAAAGCAATTTGACCTGAGACTCCATATATT 406
 QY 301 CAGATCAAGGACCAAGGCTTGTATCAATGTTTGTCTTCAATTAAGGCCCCCAAGGATC 360
 Db 407 CAGATCAAGGACCAAGGCTTGTATCAATGTTTGTCTTCAATTAAGGCCCCCAAGGATG 466
 QY 361 GTTCCCATGCGCAGATGATGATTCCTGATGAGTGTGCTTCACTTCACTGATCAAGTGA 420
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 QY 481 ATACAAGTGTACCGCAAGAACCCAGAGAGATGATTTTGGTATTAATTAACAGAGAACTCAAGT 540
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 QY 541 ACTAAGTATGATCTGTCTGATGAAGAAATCTCAAAATAATGTCACAGAACTCAAGAGCTT 600
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 Db 704 TCCATGAGCTTGTCTTCTCACTCCCTGAGTGTGAGCAAAATATACCATCTTCTGTATT 763
 QY 658 CTGCACTTGAGTCATGATGAAGCTTCCCTCACTTATATATATGATGATCAATGAGAA 717
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 QY 718 CCCACCCCTGATGAGACCAATCTCTGATGAGGCTCTGCTGTGTAATGTTGTCATT 777
 Db 821 CCTCAGCCTCCCCAGCACCACATCTCTTGATTAACAGCTGTACTTCCAA---CAGTATT 877
 QY 778 TTGTGGGATGGTGTCTTTCTTACACTAAGAAA---AGGAAGAAGACGACCTGGC 834
 Db 878 ATATGTGTGATGGTTTCTGTCTAATCTCTATGMAATGMAAAGAAAGAACGCGCTCGC 937
 QY 835 CCCCTCATGATGTGAACCAACAAAGTGAAGAAAGAAAGTGAAGACGACCAAGAA 894
 Db 938 AACCTTATATATGTGGAAACCAACACATGAGAGAGATGAACGACCAAGAA 997
 QY 895 AGAGTAGGACATGATAAGAGATCTGATGAAGCCAGTGTG---TTAACAATTTCG 951
 Db 998 AGAAGAAAATCCATATACCTGAAGATCTGATGAAGCCAGCGGTGTTTTAAAGTTCG 1057
 QY 952 AAGACAGCTTCAGGCGACAACAGTACTACACAGTTT 987
 Db 1058 AAGACATCTTCATGCGACAAAAGTGATACATGTTTT 1093

RESULT 12
 US-08-205-697A-24
 ; Sequence 24, Application US/08205697A
 ; Patent No. 6218510
 ; GENERAL INFORMATION:
 ; APPLICANT: Sharpe, Arlene H.
 ; APPLICANT: Borriello, Francescopaulo
 ; APPLICANT: Freeman, Gordon J.

Db 704 TCCATCAGCTTCTGTTTCATTCCTGATGTAGAGACATATACCATCTTCTGTAAT 763
QY 658 CTGCAACTTGATCATGATGAAAGCTTCCCTCCATCTATATATATGATGACATACGAAA 717
Db 764 CTGGAAGACGACAAAGAGCGGGCTTTATCTTACCTTCTCTATAGA---GCTTAGAGAC 820
QY 718 CCCACCCCTGATGAGACACATCTCTGATTTGGGCTCTGCTTGTATGTGTCATT 777
Db 821 CCTCAGCCCTCCCGACACATCTCTTGATGTAGAGTACAGCTTCCAA---CACTTAT 877
QY 778 TTGTGGGATGCTGCTTCTTCTTACACTAGAAA---AGAGAGACAGACGCTGCG 834
Db 878 ATATGTGATGCTGCTTCTTCTTATCTATGGAATGGAAGAAAGAGAGCGGCTCGC 937
QY 835 CCCCTCATGATGTGAACACCAACAACTGGAGAGAAAGAGAGACACCAAGAA 894
Db 938 AACTCTTATATGATGAGACACACATGAGAGAGAGAGAGATGACAGACCAAGAAA 997
QY 895 AGAGTACGCTACATGAAGAGGAAAGATCTGATGAAGCCAGTGTG---TTACATTTTCG 951
Db 998 AGAGAAAAATCCATATCTGAAAGATCTGATGAAGCCAGCGTGTTTTAAAGTTTCG 1057
QY 952 AAGACAGCTTCAGGCGACAAAGTACTACAGATT 987
Db 1058 AAGACATCTTCTGCGACAAAGTATACATGTTT 1093

RESULT 10
US-08-403-253A-3
Sequence 3, Application US/08403253A
Patent No. 6352694

GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Renner, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,253A
FILING DATE: March 10, 1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433

FILING DATE: 23 NOV 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-403-253A-3

Query Match 58.3%; Score 575.2; DB 4; Length 1120;
Best Local Similarity 77.8%; Pred. No. 1.7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

QY 1 ATGTATCTCAGATCGACTATGAACTGAATTAACATTCCTTTGATGACCCCTCGCTC 60
Db 107 ATGATGCCAGTGCAGCTATGAGCATGATGATTCCTTTGATGACCTTCCTGCTC 166
QY 61 TATGTGCTGCTTCCATGATGAGTCAAGCATATTTTCAACAGACTGAGAGACTGCCATGC 120
Db 167 TCTGTGCTGCTCCTCTGAAATTCAGCTTATTTCAATGAGACTGACAGACTGCCATGC 226
QY 121 CATTTACAATTCCTCAAAAACATAAGCCGATGATGATGATGATGATGATGATGATGATG 180
Db 227 CAATTTGCAACTCTTAAACCAACAAAGCTGAGTGTGATGATGATGATGATGATGATGATG 286
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QY 241 AAGTATAGAGGCGCGCAAGCTTTGCAAAAGACATTTGACCTGAGCTCATATATAT 300
Db 347 AAGTATAGAGGCGCGCAAGCTTTGCAAAAGACATTTGACCTGAGCTCATATATAT 406
QY 301 CAGATCAAGAGCAAGGCTTGTATCATGTTTGGTTCATCATTAAGAGGCGCAAGAGCTC 360
Db 407 CAGATCAAGAGCAAGGCTTGTATCATGTTTGGTTCATCATTAAGAGGCGCAAGAGCTC 466
QY 361 GTTCCATGACCAAGATGATTTGACCTATGACCTGATGATGATGATGATGATGATGATG 420
Db 467 ATTCGATCACCAGATGATTTCTGAATCTGACAGTGTGCTGATGATGATGATGATGATG 526
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Db 644 ATCGAGTATGATGATGATGAGAAATCTCAAAATATGTCACAGACTGTACAGCTT 703
QY 601 TCTATCAGCTTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
Db 704 TCTATCAGCTTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 763
QY 658 CTGCAACTTGATCATGATGAAAGCTTCCCTCCATCTATATATATGATGACATACGAAA 717
Db 764 CTGGAAGACGACAAAGAGCGGGCTTTATCTTACCTTCTCTATAGA---GCTTAGAGAC 820
QY 718 CCCACCCCTGATGAGACACATCTCTGATTTGGGCTCTGCTTGTATGTGTCATT 777


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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 347 AAGTATATGGCGCGCAAGTTTGATTCGGACAGTTGGACCCCTAGACCTTCACAACTCTT 406
Oy 301 CAGATCAAGGACAAAGGCTTGATCAAGTTTCGTTCAATCAATAAGGCCCAAGGACTC 360
Db 407 CAGATCAAGGACAAAGGCTTGATCAAGTTTCATCATTCATCAACAAAAGGCCACAGAAATG 466
Oy 361 GTTCCCATGACCAAGATGAAATTCAGCTATGACGCTTGCTGAATTCAGTCAACCTGAA 420
Db 467 ATTGGATCCACCAAGATGAAATTCAGCTATGACGCTTGCTGAATTCAGTCAACCTGAA 526
Oy 421 ATATGTAATCTTCAATAGAACAGAAATTCGATCATCAATTAATTTGACCTGCTCATCC 480
Db 527 ATATGTAATCTTCAATAGAACAGAAATTCGATCATCAATTAATTTGACCTGCTCATCT 583
Oy 481 ATACAAAGTTACCCAGAACCCCAAGAGATGTATTTTGGTAAAAACCGAGATTCAGT 540
Db 584 ATACAGGTTTACCCAGAACCCCAAGAGATGTATTTTGGTAAAAACCGAGATTCAGT 643
Oy 541 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATATGTCAGAGAACTCTACAGCTT 600
Db 644 ATGAGTATGATGTATTAATGAGAAATCTCAAGATATGTCAGAGAACTCTACAGCTT 703
Oy 601 TCTATCAGCTTGCTCTCTCAGTCCCTGAAG--CAAGCAATGTGACATCTTCTGTCTC 657
Db 704 TCCATCAGCTTGCTCTCTCAGTCCCTGAAG--CAAGCAATGTGACATCTTCTGTCTT 763
Oy 658 CTGCAACTGTAGTCAATGAAGCTTCCCTCCTTACCTTAATATATGATGACATAGAA 717
Db 764 CTGGAACCTGTAGTCAATGAAGCTTCCCTCCTTACCTTCTCTATGAA--GCTTGAGAC 820
Oy 718 CCGACCCCTGATGAGACCATCTCTGTGATGCGGCTCTGCTGTATGTTGTCAT 777
Db 821 CCGACCCCTGATGAGACCATCTCTGTGATGCGGCTCTGCTGTATGTTGTCAT 877
Oy 778 TTGTGGGATGTGTCTTCTTCTAACAATAAGGAA--AGGAAGAAGACAGCTGCTC 834
Db 878 ATATGATGTGTGTCTTCTTCTAACAATAAGGAA--AGGAAGAAGACAGCTGCTC 937
Oy 835 CCGCTCATATATGTGAACCAACAAGTGAAGGAAAGAAAGAAATGAGACCAAGGAA 894
Db 938 AACTCTTATATATGTGAACCAACAAGTGAAGGAAAGAAAGAAATGAGACCAAGGAA 997
Oy 895 AGAGTACGATCATGTAAGGAAAGATGTGAAGGCCAGTGTG--TTAACAATTTG 951
Db 998 AGAGTACGATCATGTAAGGAAAGATGTGAAGGCCAGTGTG--TTAACAATTTG 1057
Oy 952 AAGACGCTTCAGGCGACAAACAGTACTACAGCTT 987
Db 1058 AAGACGCTTCAGGCGACAAACAGTACTACAGCTT 1093

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RESULT 9
US-08-702-525-22
; Sequence 22, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Borriello, Francescopolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER, READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BMI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-702-525-22

Query Match 58.3% Score 575.2; DB 4; Length 1120;
Best Local Similarity 77.8%; Pred. No. 1.7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

Oy 1 ATGATCTCAGATGCACTATGGAATGAATCAATCTCTTTGTGATGACCTCTCTC 60
Db 107 ATGATGCCCAAGTGACATATGAGGACTGATGAACATCTCTTTGTGATGACCTCTCTC 166
Oy 61 TATGTCGTCTCTCATTAAGATCAAGCATATTTCAACAAGACTGAGAACTGATGC 120
Db 167 TCTGTGCTGCTCTCTCAAGATTCATCAATTTCAATGAGAGCTGACAGCTCTCAGTC 226
Oy 121 CATTTTACAATTTCAAAACATTAAGCCTGATGATGATGTGTGTTGGCAGACCAG 180
Db 227 CATTTTCAAACTCTCAAAACCAAAAGCCTGATGATGATGTGTGTTGGCAGACCAG 286
Oy 181 GATAAGCTGCTCTCTATAGAGCTATACAGAGCAAGAAAGAAAGCCCAAAATGTTCAATGC 240
Db 287 GAAACTGCTCTCTGAATAGAGTATATTAGGCAAGAGAAATTTGACAGTTCATTC 346
Oy 241 AAGTATAGGCGCGACAAAGCTTTGACAAAGCAATTTGACCCGAGACCTCATTAATTT 300
Db 347 AAGTATAGGCGCGCGACAAAGCTTTGATTCGACAGCTTTGACCCGAGACCTCATTAATTT 406
Oy 301 CAGATCAAGGACAAAGGCTTGATCAATGTTTCGTTCAATTAAGGCGCCCAAGGACTC 360
Db 407 CAGATCAAGGACAAAGGCTTGATCAATGTTTCATCATTCATCAACAAAAGGCCACAGAAATG 466
Oy 361 GTTCCCATGACCAAGATGAAATTCAGCTATGACGCTTGCTGAATTCAGTCAACCTGAA 420
Db 467 ATTGGATCCACCAAGATGAAATTCAGCTATGACGCTTGCTGAATTCAGTCAACCTGAA 526
Oy 421 ATATGTAATCTTCAATAGAACAGAAATTCGATCATCAATTAATTTGACCTGCTCATCC 480
Db 527 ATATGTAATCTTCAATAGAACAGAAATTCGATCATCAATTAATTTGACCTGCTCATCT 583
Oy 481 ATACAAAGTTACCCAGAACCCCAAGAGATGTATTTTGGTAAAAACCGAGATTCAGT 540
Db 584 ATACAGGTTTACCCAGAACCCCAAGAGATGTATTTTGGTAAAAACCGAGATTCAGT 643
Oy 541 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATATGTCAGAGAACTCTACAGCTT 600
Db 644 ATGAGTATGATGTATTAATGAGAAATCTCAAGATATGTCAGAGAACTCTACAGCTT 703
Oy 601 TCTATCAGCTTGCTCTCTCAGTCCCTGAAG--CAAGCAATGTGACATCTTCTGTCTC 657

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MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-280-757B-1

Query Match 58.38; Score 575.2; DB 3; Length 1120:
Best Local Similarity 77.88; Pred. No. 1.7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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OY 1 ATGTATCTCAATGACATATGAACTGAATACATCTCTTTGTGATGACCTCTGCTC 60
DB 107 ATGATCCCACTGACATATGAGTAACTCTCTTTGTGATGAGCTCTGCTC 166
OY 61 TATGTCGTCCTCCATGAAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
DB 167 TCTGTCGTCCTCCATGAAGTCAAGCTTATTTCAATGAGTCAAGCTGAGACCTGCCATGC 226
OY 121 CATTTTAAATTTCCAAACATTAAGCTTGATGATGTTGGTGGACGACAG 180
DB 227 CATTTTGAACCTGCAAAACCAAGCCTGATGAGTATGATTTTGGACGACAG 286
OY 181 GATAAGCTGTTCTGTACAGACTATACAGAGCAAGAACCTCAAAATGTTCAATCC 240
DB 287 GAAACCTGTTCTGAAATGAGTATCTTAAAGCAAGAAATTTGACAGTGTTCATTC 346
OY 241 AAGTAAAGGGCCGACAAAGCTTTGACAAAGCAATTTGAGACCTGACATCAATAT 300
DB 347 AAGTAAAGGGCCGACAAAGCTTTGATTTGACAGCTTTGACACCTGACATCAAT 406
OY 301 CAGATCAAGCAAGAGGCTTATCATATGTTGTTGTCATATAAAGGCCCAAGACATC 360
DB 407 CAGATCAAGCAAGAGGCTTATCATATGTTGTCATATAAAGGCCCAAGAGATG 466
OY 361 GTTCCACGACACGAGTAAATTCGACATTCAGTGTCTGTAATCTCAGTCAACCGAA 420
DB 467 ATTCCATCCACGAGATTAATTCGAGTGTGACATGCTTGTGTAATCTCAGTCAACCGAA 526
OY 421 ATTAATGTAATCTCTTAATAGAAGAAATTTGCGCATCAATTAATTTGACCTGCTCATCC 480
DB 527 ATAGTACCAATTTCTAAATATACAGAAAA--TGTGTACATTAATTTGACCTGCTCATCT 583
OY 481 ATACAAGGTTTCCGACAGACGAGAGATGATTTTGTGTAAGAACCGGAATTCAGT 540
DB 584 ATACAGGTTTCCGACAGACGAGAGATGATTTTGTGTAAGAACCGGAATTCAGT 643
OY 541 ACTAATGTAATCTCTTAATAGAAGAAATTCGCAATATGTCACAGAACTCTACACGTT 600
DB 644 ATCGAGTATGATGATATATGCAAAATTCAGATATATGTCACAGAACTGTACAGCTT 703
OY 601 TCTATCAGCTGTCTCTTCTGACGCTCGAAG--CAAGCAATGAGACATCTCTGCTC 657
DB 704 TCCATCAGCTGTCTCTTCTGACGCTCGAAG--CAAGCAATGAGACATCTCTGCTC 763
OY 658 CTGCAACTTGAATCAATGAAGCTTCCCTCCTCACTATATAATATAGTGCATACGAAA 717
DB 764 CTGCAACTTGAATCAATGAAGCTTCCCTCCTCACTATATAATATAGTGCATACGAAA 820
OY 718 CCCACCTCTGATGAGACCAATCTCTGATTTGCGGCTGCTGCTTGAATGTTGCTCAT 777
DB 821 CCTCAGCTCTCCCGACACATCTCTGATTTGAGTATGACGTGACTTCCAA--CAGTAT 877
OY 778 TTGTGTTGAGTGTGTTCTTTCTTAACACTAGAGAA--AGSAGAGAGAGACCTGCGC 834
DB 878 ATATGTTGAGTGTGTTCTTTCTTAACACTAGAGAA--AGSAGAGAGAGACCTGCGC 937
OY 835 CCTCTCATGATGTTGAACCAAGAGTGAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 894
DB 938 AACTCTTAAATGTTGAACCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 997
OY 895 AAGTAAAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
DB 998 AAGTAAAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1057
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OY 952 AAGACAGCTTCAGGCGACCAACAGTACTACACAGTTT 987
DB 1058 AAGACATCTTCATCGCAGCAAAAGTATACATGTTT 1093

RESULT 8
US-08-205-697A-22
Sequence 22, Application US/08205697A
Patent No. 6218510

GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.

APPLICANT: Nadler, Lee M.

TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BMI-120

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs

TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:
NAME/KEY: CDS

LOCATION: 107..1093

US-08-205-697A-22

Query Match 58.38; Score 575.2; DB 4; Length 1120:
Best Local Similarity 77.88; Pred. No. 1.7e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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OY 1 ATGTATCTCAATGACATATGAACTGAATACATCTCTTTGTGATGACCTCTGCTC 60
DB 107 ATGATCCCACTGACATATGAGTAACTCTCTTTGTGATGAGCTCTGCTC 166
OY 61 TATGTCGTCCTCCATGAAGTCAAGCATATTTCAACAAGACTGAGAACTGCCATGC 120
DB 167 TCTGTCGTCCTCCATGAAGTCAAGCTTATTTCAATGAGTCAAGCTGAGACCTGCCATGC 226
OY 121 CATTTTAAATTTCCAAACATTAAGCTTGATGATGTTGGTGGACGACAG 180
DB 227 CATTTTGAACCTGCAAAACCAAGCCTGATGAGTATGATTTTGGACGACAG 286
OY 181 GATAAGCTGTTCTGTACAGCTATACAGAGCAAGAGAACCTCAAAATGTTCAATCC 240
DB 287 GAAACCTGTTCTGAAATGAGTATCTTACGCAAGAGAAATTTGACAGTGTTCATTC 346
OY 241 AAGTAAAGGCGCCGACCAAGCTTTGACAAAGACAAATTTGAGACCTGAGACTTCATAT 300
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APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1120 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1093
US-08-479-744A-1

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Query Match      58.3%  Score 575.2: DB 3: Length 1120:
Best Local Similarity 77.8%  Pred. No. 1,7e-165:
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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OY 1 ATGTATCTCAGATGACATGTAAGTGAATTAACATTTCTTTGTGATGACCTCTGCTC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 107 ATGATGATCCCATGCTGATGGAGTGAATGATGATGATGATGATGATGATGATGATG 165
OY 61 TATGTCGCTGCTTCATGTAAGTGAATGATGATGATGATGATGATGATGATGATGATG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 TCTGTCGCTGCTTCATGTAAGTGAATGATGATGATGATGATGATGATGATGATGATG 226
OY 121 CATTTTACAAATCTCAAAACATAGCTGATGATGATGATGATGATGATGATGATGATG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 CATTTTGCACAACTCTCAAAACATAGCTGATGATGATGATGATGATGATGATGATGATG 286
OY 181 GATTAAGCTGCTTCTGATGACGCTATACAGAGCAAGCAAGCAAGCAAGCAAGCAAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 GAAACCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 346
OY 241 AATTAATAGGCGCGACAGCTTGCACAAAGCAATGACCTGACGATCATATATAT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 AAGTATATGCGCGACAGCTTGCACAAAGCAATGACCTGACGATCATATATAT 406
OY 301 CAGATCAAGCAAGGAGCTTGTATCAATGTTTCTCATCATTAAGGCGCAAGGAGCTC 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 407 CAGATCAAGCAAGGAGCTTGTATCAATGTTTCTCATCATTAAGGCGCAAGGAGCTC 466
OY 361 GTTCCCATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 467 ATTGAGATCCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 526
OY 421 ATATAGTACTCTCTATATAGACAGAAATTTCTGGCATCATTAATTTGACCTCTCATGC 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 527 ATAGTACCAATTTCTATATATACAGAAAA---TGTGATCATTAATTTGACCTCTCATGC 583
OY 481 ATCAAGGTTACCAAGCAAGCAAGATGATGATGATGATGATGATGATGATGATGATG 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 584 ATCAAGGTTACCAAGCAAGCAAGATGATGATGATGATGATGATGATGATGATGATG 643
OY 541 ACTAATATATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 644 ATCAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 703
OY 601 TCTATCAGCTTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 704 TCCATCAGCTTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 763

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OY 658 CTGCAACTTGAGTCAATGAAAGCTTCCCTCCCTACCTTATATATAGATCACAATAGAAA 717
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DB 764 CTGGAACCTGACAAAGAGCGGCTTTATCTTACCTTCTATATAGA---GCTTGAGGAC 820
OY 718 CCACACCCCTATGAGACACACATTCCTGATGATGCGGCTCTGTTTATGTTGGCAT 777
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 CCTGAGCCTCCCGACACCATCTCTGATGATGATGATGATGATGATGATGATGATG 877
OY 778 TTGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 834
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 878 ATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 937
OY 835 CCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 938 AACTCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 997
OY 895 AGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 998 AGAGAAAAATCCATATACCTGAAAGATGATGATGATGATGATGATGATGATGATG 1057
OY 952 AAGACGCTTCAGCGACGACAGTACTACAGATTT 987
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1058 AAGCATCTTCATGCGACAAAGATGATGATGATTT 1093

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RESULT 7
US-08-280-757B-1
; Sequence 1, Application us/08280757B
; Patent No. 6130316
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; APPLICANT: Greenfield, Edward
; TITLE OF INVENTION: No. 6130316el CTLA4/CD28 ligands and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: us/08/280,757B
; FILING DATE: 26-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624
; FILING DATE: 26-JULY-1993
; APPLICATION NUMBER: 08/109,393
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: 08/147,773
; FILING DATE: 3-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

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;
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: No. 5942607e1 CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
; US-08-101-624-1

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Query Match 58.3%; Score 575.2; DB 2; Length 1120;

Best Local Similarity 77.8%; Pred. No. 1,7e-165; Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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QY 1 ATGTATCTAGATGCACTATGGAATGTAATCAATTCCTTTGTGATGACCCCTCTCTC 60
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DB 107 ATGATGCCCACTGCACTATGGACTGATGAACATTCCTTTGTGATGACCCCTCTCTC 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TATGCTGCTCTTCATGAGAGTCAGCATATTTCAACAAGACTGGAGACTGCCATGC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 TCTGGTGCCTCTCTGTAAGATTCACCTTATTTCAATGAGACTGCAGACCTCCATGC 226
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 CATTTACAAATTCACAAACATTAAGCCTGATGAGTGGTGTAGTTGGCAGAGCAG 180
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DB 227 CAATTTGCAAACTCTCAAAACCAAGCCTGAGTGAAGTATTTTGGCAGAGCAG 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GATTAAGCTGCTTCTGTACAGCTATACAGAGGCAAGAAGACCTCAAAATGTTCAATGC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 GAAACCTTGCTCTGAATGAGGTATATAGGCAAGAAATTTGACAGTGTCAATTC 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AAGTATTAAGGGCGCACAACTTTGACAAAGCATTTGAGCCCGAGAGCTCCATATATTT 300
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DB 347 AAGTATTAAGGGCGCACAACTTTTATTTGAGAGTGGACCCCTGAGACTTCAATCTT 406
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 CAGATCAAGAGCAGAGGCTTGTATCAATGTTTGTTCATTAAGGCGCCCAAGAGACTC 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 407 CAGATCAAGAGCAGAGGCTTGTATCAATGATTCATCAACAAAAGCCACAGAGATG 466
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 GTTCCATGACCAAGATGATTCAGCTATTCAGTGTCTGTAATTCAGTCAACCTGAA 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 467 ATTGCATCCACCAAGATGATTCCTGAACCTGCTGCTGCTGCTGCTGCTGCTGCAACCTGAA 526
QY 421 ATATGTAATCTCTTAATAGACAGAAAATTTGGCATTCATTAATTTGACCTGCTCATCC 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 527 ATAGTACCAATTTCTAATATACAGAAA---TGTGTACATTAATTTGACCTGCTCATCT 583
QY 481 ATACAGGTTACCCAGAACCCAGAGATGATTTTGGTAAAAAAGGATTCAGT 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 584 ATACAGGTTACCCAGAACCTTAAGAGATGAGTGTTTTGGCTAAGAACCAAGAAATTCAC 643
QY 541 ACTAAGTATGATGCTGCTCATSAAGAAATCTCAAAATATGTACAGAACTCTCAACGTT 600
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DB 644 ATGAGTATGATGATATATGACAGAAATCTCAAGATATGACAGAACTGACGAGCTT 703
QY 601 TGTATCAGCTTGTCTCTTCAGTCCCGAAG---CAGCAATGTGACCATCTCTGTGC 657
DB 704 TGTATCAGCTTGTCTCTTCATTCCTGATGTATGAGCAATATGACCATCTCTGTAT 763
QY 658 CTGCAACTGTGAGTCATGATGACCTTCCCTCCCTACCTTATATATGATGACATAGGAA 717
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 764 CTGGAAGTGAACAGACGCGGCTTTTATCTTCACTTCTCTATAGA---GCTTGAGGAC 820
QY 718 CCCACCCCTGATGAGACACACATCTCTGATTCGCGCTGCTGTTGATGTGTCAT 777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 821 CCTCAGCCTCCCGACACACATTCCTTGATTTACAGCTGACTTCCAA---CAGTTATT 877
QY 778 TTGTGTGGATGCTGCTTCTTCTTAACACTAGGAA---AGAGAGAGAGACGCTGCG 834
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DB 878 ATATGTGATGATGTTTCTGTCTAATTTCTATGAAATGGAAGAGAGAGCGGCTCGC 927
QY 835 CCTCTCATGATGTGAACCAACAAAGTGAAGAGAAAGAACTGACGACACAGGAA 894
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DB 938 AACCTTTAATGATGGAACCAACACATGAGAGAGAGAGAGTGAACAGACCAAGAA 997
QY 895 AGAGTACGCTACCATGAAGAAAGATCTGATGAAGCCAGCTG---TTACATTTGC 951
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DB 998 AGAGAAAAATCATATATCTGTAAGATCTGATGAGCCGAGCGCTGTTTTAAAGTTGC 1057
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DB 1058 AAGACATCTTCATGCGACAAAAGTATGATGATTTT 1093

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RESULT 6

US-08-479-744A-1

; Sequence 1, Application US/08479744A

; Patent No. 6084067

; GENERAL INFORMATION:

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: No. 6084067e1 CTLA4/CD28 Ligands and

; TITLE OF INVENTION: Uses Therefor

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/479,744A

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/280,757

; FILING DATE: 26-JUL-1994

Oy	778	TTTGTTGGGATGGGTTCTCTTTCTAACTAGAGAA---AGGAAGAAGAAAGCCCTGGC	834
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Db	838	AACCTCTTAATATGTGGAACCAACCAATGGAAGGGAAGAGATGAACAGACCAAGAA	897
Oy	895	AGAGTACGGTCCATGAAACGGAAGATCTGATGAAGCCCACTGTG---TTAACAATTTCG	951
Db	898	AGAGAAAAAATCCATATCTACCTGGAAGAATCTCATGAAGCCCAAGCTGTTTTAAAGATTGC	957
Oy	952	AAGAGGCTTCAGGGAACAACAGTACACAGTTT	987
Db	958	AAGACATCTTCATGCGACAAAGATGATCACTGTTT	993

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      1  RESULT 4
      2  US-08-456-104-1
      3  / Sequence 1, Application US/08456104
      4  / Patent No. 5861310
      5  /
      6  / GENERAL INFORMATION:
      7  /
      8  / APPLICANT: Freeman, Gordon J.
      9  /
     10  / APPLICANT: Nadler, Lee M.
     11  /
     12  / TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
     13  / NUMBER OF SEQUENCES: 8
     14  /
     15  / CORRESPONDENCE ADDRESS:
     16  / ADDRESSEE: LAHIVE & COCKFIELD
     17  / STREET: 60 State Street, Suite 510
     18  /
     19  / City: Boston
     20  /
     21  / STATE: Massachusetts
     22  /
     23  / COUNTRY: USA
     24  /
     25  / ZIP: 02109
     26  /
     27  / COMPUTER READABLE FORM:
     28  /
     29  / MEDIUM TYPE: Floppy disk
     30  /
     31  / COMPUTER: IBM PC compatible
     32  /
     33  / OPERATING SYSTEM: PC-DOS/MS-DOS
     34  /
     35  / SOFTWARE: PatentIn Release #1.0, Version #1.25
     36  /
     37  / CURRENT APPLICATION DATA:
     38  /
     39  / APPLICATION NUMBER: US/08/456,104
     40  /
     41  / FILING DATE:
     42  /
     43  / CLASSIFICATION: 424
     44  /
     45  / PRIOR APPLICATION DATA:
     46  /
     47  / APPLICATION NUMBER: 08/101,624;
     48  /
     49  / FILING DATE: 26-JUL-1993;
     50  /
     51  / APPLICATION NUMBER: 08/109,393;
     52  /
     53  / APPLICATION NUMBER: 19-AUG-1993
     54  /
     55  / ATTORNEY/AGENT INFORMATION:
     56  /
     57  / NAME: Mandragouras, Amy E.
     58  /
     59  / REGISTRATION NUMBER: 36,207
     60  /
     61  / REFERENCE/DOCKET NUMBER: RPI-008
     62  /
     63  / TELECOMMUNICATION INFORMATION:
     64  /
     65  / TELEPHONE: (617) 227-7400
     66  /
     67  / TELEFAX: (617) 227-5941
     68  /
     69  / INFORMATION FOR SEQ ID NO: 1:
     70  /
     71  / SEQUENCE CHARACTERISTICS:
     72  /
     73  / LENGTH: 1120 base pairs
     74  /
     75  / TYPE: nucleic acid
     76  /
     77  / STRANDEDNESS: single
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     79  / TOPOLOGY: linear
     80  /
     81  / MOLECULE TYPE: cDNA
     82  /
     83  / FEATURE:
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     85  / NAME/KEY: CDS
     86  /
     87  / LOCATION: 107..1093
     88  /
     89  / US-08-456-104-1

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Query Match	58.3%	Score 575.2;	DB 2,	Length 1120;
Best Local Similarity	77.8%	Pred. No. 1,7e+15;		
Matches 775; Conservative		0; Mismatches 203;	Indels 18;	Gaps 6;

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Db	167	TCTGGTGTGCTCTCTCGAAGATTCAGCAAGCTATTATTTAAATGAGACTGCAACCTGGCATGC	226
Qy	121	CATTTCACAAATTTCCAAACATATAGCGCTGATGAGTGTGATGTGTTTGGCAGCAGCAG	180
Db	227	CAATTTGCCAAACTCTCAAAAACCAAGCGCTAGAGACTAGTAGTATTTTTGGCAGGACGAC	286
Qy	181	GATAAGCTGTTTCTGTACGAGCTATACAGAGGCAAGAGAAAGAACCCCTCAAAATGTCATGCC	240
Db	287	GAAACTGTGTTGTGATGAGGTATACCTTAGCGAAAGAGAAATTTAGCAGTGTCAATTCC	346
Qy	241	AAGTATAAAGGCGCCGACAAAGCTTTGACAAAGACAATTTGAGCCCTGAGACTCCATTAATNT	300
Db	347	AAGTATAGGCGCCGACAAAGTTTTTGTATCGCAAGTTGGACCGCTGAGACTTCACATCTT	406
Qy	301	CAGATCAAGGACAAAGGCGCTGTATCAATGTTTGTCATCATATAAAGGCGCCAAAGAGATC	360
Db	407	CAGATCAAGGACAAAGGCGCTGTATCAATGATATATCATCATACAAAAGCCACAGGAATG	466
Qy	361	GTTCCCATGACCAAGATGAATTCGTACAGTTCAGTGCCTGCTTACTTCAGTCAACCTGAA	420
Db	467	ATTGCCATCCACAGATGAATTTGCACTGTCACTGCTGTTCTTACTTCAGTCAACCTGAA	526
Qy	421	ATTAATGTAATCTTCTAATAGAACGAAATTTGCGCATCATTAATTGAGCGTGCATCC	480
Db	527	ATAGTACCAATTTCTAATATACAGAAAA--TGTCATCAATTAATTGACCTGCTCATCT	583
Qy	481	ATACAGAGTTCACCCAGAACCCCAAGAGATGTATTTTGGTAAAAAACGAGAAATTCACCT	540
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Qy	541	ACTAAGTATGATCTGTCATGAGAGAAATTCACAAATATATCTCACAGAACTCTACAACTT	600
Db	644	ATCGATGTATGATGTATATATGCAAAAATCTCAGATATATCTCACAGAACTGTACGACGTT	703
Qy	601	TCTATACACTGTCTCTCTCGTACGTCCTCGAAG--CAAGCAATGTGAGCAATCTCTGTC	657
Db	704	TCTATACACTGTCT	763
Qy	658	CTGCAACTGTGATCAATGAAGCTTCCCTCCCTCACTTATATATAGATGCATACAGAA	717
Db	764	CTGGAAGTCTGACAAAGACCGCGCTTTATCTTCACTTCTCTCTCTCTCTCTCTCTCTCTCT	820
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Db	821	CCCTGACCTCCCCAGACCAACATCTCTGATCTATACAGTCTACTTCTCTCTCTCTCTCTCT	877
Qy	778	TGTGTGGGATGTGTCTTCTCTTAACACTAAGAAA--AGSAAAGAAAGACGCTGGC	834
Db	878	ATATGTGTGATGTGTCTTCTCTAATCTTAAGGAAAAAGSAAAGAAAGACGCGCTGCG	937
Qy	835	CCCTCTCATGTATGGAACCAACAAAGTGGAGAAAGAAAGAAAGTGGAGCAACCAAGAA	894
Db	938	AACCTTATTAATGTGTGAGAACCAACACATGSAAGAGGGAAGAGATGTGAACGACCAAGAA	997
Qy	895	AGAGTACGGTACATGAAGAGGAAAGATCTGTATGAGAGCCAGTGTC--TTAATCTTGG	951
Db	998	AGAGAAAAAATCATATATACCTGGAAGAGATCTGTATGAGAGCCAGCGTGTTTTAAAGTTGG	1051
Qy	952	AAGACAGCTTCAGGTGACACAAAGTATACACATCTT	987
Db	1058	AAGACATCTTCATGTGCAACAAAGTATACATGTTT	1093

RESULT 5
US-08-101-624-1
; Sequence 1, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.

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Db      367 ATTGCATCCACAGATGAATTCGAACTGTCAGTGGCTGGTAACCTGACCACTGAA 428
OY      421 ATAAAGGTAACTCTCTAATATGAAACAGAAAAATTCCTGGCATCATAAATTGACCTGCTATCC 480
Db      427 ATATGTACCAATTTCTAAATATAACAGAAAA---TGTTGATCAATAAATTGACCTGCTCATCT 483
OY      481 ATACAAAGGTACCCAGAAACCCAGAGAGATGTATTTTGGTAAAAACCGAGAAATTCAGT 540
Db      484 ATACAGGGTATCCAGAAACCTAAGAAAGATGATGTTTTTGGCTAAACCAAGAAATTCACCT 543
OY      541 ACTAAGTATGATACGTCTATGATGAGAAATCTCAAAATTAATATGTCACAGAACTCTACACGTT 600
Db      544 ATCGGATATGATGATTAATATGACGAAATCTCAAGATATATGATCAAGAACTGTACGACGTT 603
OY      601 TCTATCAGCTTCTCCTCTCATGTCCTCCCTGAAG---CAAGCAATGTGACATCTTCTGTGC 657
Db      604 TCCATCAGCTGTCTGTTCTTCAATCCCTGATGTATGACAGCAATATGACCACTTCTCTGATT 663
OY      658 CTGCAACTTGAATCATATGAGCTTCCCTCCCTCACTTATATATATAGATGACATACGAAA 717
Db      664 CTGGAACCTGCACAAAGCCGCGCTTTATCTTCACCTTCTCTATAGA---GCTTAGAGAC 720
OY      718 CCCACCCCTGATGGAGACACATCCTCTGAGTTGCGGCTCTGCTTGAATGTTGTCATT 777
Db      721 CCTCAGCCTCCCCCAGACCAATCTCTTGATGATACAGCTGACTTCCAA---CAGTATT 777
OY      778 TTGTGTGGATGTGTGTTCTTCTTAACACTAAGAAA---AGAAAGAAAGACAGCCGCGC 834
Db      778 ATATGTGATGATGTTTCTGTCTAATCTATGAGAAATGAGAAAGAAAGAACGCGCTCGC 837
OY      835 CCTCTCATGATGTGAAACCAACAAAGTGGAGAGAAAGAAAGTGAAGCAGACCAAGAA 894
Db      838 AACTCTTAAATATGGAACCAACACATGTGAGGGAGAGAGTGAACAGACAAGAA 897
OY      895 AGAGTAGCTGTCCATGAAACGGAAGATCTGATGAAGCCAGATG---TTACATTTCG 951
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OY      952 AAGACAGCTTCAAGCCGACACACAGTACTACACAGTTT 987
Db      958 AAGACATCTTCATGCGACAAAAAGTATACATGTTTT 993

RESULT 3
US-09-762A-33
Sequence 33, Application US/09039762A
Patent No. 6255073
GENERAL INFORMATION:
APPLICANT: Cai, Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6255073th Wacker Drive, 36th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,762A
FILING DATE: 16-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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Query Match	Best Local Similarity	Matches 775; Conservative	Score 575.2; DB 4;	Length 1002;
NAME: OLSON, Arne M.	77.8%;	0;	203;	
REGISTRATION NUMBER: 30,203				
REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV. 2				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: (312) 580-1180				
TELEFAX: (312) 580-1189				
INFORMATION FOR SEQ. ID NO: 33:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 1002 base pairs				
TYPE: nucleic acid				
STRANDEDNESS: double				
TOPOLOGY: linear				
MOLECULE TYPE: CDNA				
HYPOTHETICAL: NO				
ANTI-SENSE: NO				
US-09-039-762A-33				
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Best Local Similarity	77.8%;	Pred. No. 1.6e-165;		
Matches 775; Conservative	0;	Mismatches 203;	Indels 18;	Gaps 6
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QY 952 AAGACAGCTTCAAGGCAAGGCTTTGATGATGATGATGATGATGATGATGATGAT 987
DB 958 AAGACAGCTTCAAGGCAAGGCTTTGATGATGATGATGATGATGATGATGATGAT 993

RESULT 2
US-09-641-33
; Sequence 33, Application US/09039641
; Patent No. 6251627

GENERAL INFORMATION:
APPLICANT: Cal. Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR
TITLE OF INVENTION: ACTIVATION OF T-CELLS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6251627th Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039, 641
FILING DATE: 8-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI4710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-641-33
Query Match 58.3%; Score 575.2; DB 4; Length 1002;
Best Local Similarity 77.8%; Pred. No. 1.6e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;
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GenCore version 5.1.3
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(without alignments)
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Sequence: 1 atgattcagatgcactat.....acaacgtactacacagttt 987

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCITUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfilest1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575.2	58.3	1002	US-09-039-982A-33	Sequence 33, Appl
2	575.2	58.3	1002	US-09-039-641-33	Sequence 33, Appl
3	575.2	58.3	1002	US-09-039-762A-33	Sequence 33, Appl
4	575.2	58.3	1120	US-08-456-104-1	Sequence 1, Appl
5	575.2	58.3	1120	US-08-101-624-1	Sequence 1, Appl
6	575.2	58.3	1120	US-08-479-744A-1	Sequence 1, Appl
7	575.2	58.3	1120	US-08-280-757B-1	Sequence 1, Appl
8	575.2	58.3	1120	US-08-205-697A-22	Sequence 22, Appl
9	575.2	58.3	1120	US-08-702-525-22	Sequence 22, Appl
10	575.2	58.3	1120	US-08-403-253A-3	Sequence 3, Appl
11	575.2	58.3	1120	PCR-US95-02576-22	Sequence 2, Appl
12	575.2	58.3	1161	US-08-205-697A-24	Sequence 24, Appl
13	575.2	58.3	1161	US-08-702-525-24	Sequence 24, Appl
14	575.2	58.3	1161	PCR-US95-02576-24	Sequence 24, Appl
15	570.2	57.8	1424	US-09-326-186B-226	Sequence 226, App
16	570.2	57.8	1428	PCR-US94-09642-1	Sequence 1, Appl
17	565.2	57.3	972	US-08-848-760B-11	Sequence 11, Appl
18	463.8	47.0	751	US-09-039-982A-34	Sequence 34, Appl
19	463.8	47.0	751	US-09-039-641-34	Sequence 34, Appl
20	463.8	47.0	751	US-09-039-762A-34	Sequence 34, Appl
21	344.4	34.9	1151	US-08-456-104-3	Sequence 3, Appl
22	344.4	34.9	1151	US-08-205-697A-20	Sequence 20, Appl
23	344.4	34.9	1151	US-08-702-525-20	Sequence 20, Appl
24	344.4	34.9	1151	PCR-US95-02576-20	Sequence 20, Appl
25	344.4	34.9	1163	US-08-479-744A-22	Sequence 22, Appl
26	344.4	34.9	1163	US-08-280-757B-22	Sequence 22, Appl
27	337.2	34.2	1261	US-08-205-697A-12	Sequence 12, Appl

28	337.2	34.2	1261	4	US-08-702-525-12	Sequence 12, Appl
29	337.2	34.2	1261	5	PCR-US95-02576-12	Sequence 12, Appl
30	232.4	23.5	330	3	US-08-479-744A-44	Sequence 44, Appl
31	232.4	23.5	330	3	US-08-280-757B-44	Sequence 44, Appl
32	175.2	17.8	306	3	US-08-479-744A-46	Sequence 46, Appl
33	175.2	17.8	306	3	US-08-280-757B-46	Sequence 46, Appl
34	103.4	10.5	210	4	US-08-205-697A-31	Sequence 31, Appl
35	103.4	10.5	210	4	US-08-702-525-31	Sequence 31, Appl
36	103.4	10.5	210	5	PCR-US95-02576-31	Sequence 31, Appl
37	45	4.6	195	4	US-08-205-697A-41	Sequence 41, Appl
38	45	4.6	195	4	US-08-702-525-41	Sequence 41, Appl
39	45	4.6	195	5	PCR-US95-02576-41	Sequence 41, Appl
40	39.4	4.0	7218	1	US-08-232-463-14	Sequence 14, Appl
41	34.6	3.5	492	2	US-08-328-111-335	Sequence 335, App
42	32.6	3.3	2747	2	US-08-874-347-1	Sequence 1, Appl
43	32.6	3.3	2747	2	US-09-093-522-1	Sequence 1, Appl
44	32.4	3.3	3341	2	US-08-868-577-18	Sequence 18, Appl
45	32.2	3.3	6216	4	US-09-415-522-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-039-982A-33
Sequence 33, Application US/09039982A
Patent No. 6225042
GENERAL INFORMATION:
APPLICANT: Cal, Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-C
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Olson & Hierl, Ltd.
STREET: 20 No. 6225042th Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-Mar-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: T5R14710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
US-09-039-982A-33

Query Match 58.3%; Score 575.2; DB 4; Length 1002;
Best local Similarity 77.8%; Pred. No. 1.6e-165;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

Db 864 AATGATATGGTGAAGACCATATAATGACACGGAAGCGAGTGTGACACAACTTAGAAGACGA 923

Oy 898 GTACGGTACCATGAACGGAAGATCTTGATGACGCCAGTG--TGTAACTTTGCGAG 954

Db 924 GCAGAGTCGCAT-----GAAGCATCTGATGATGATGCCACGATGATGTTAATATTTTAAAG 977

Oy 955 ACAGCTTCAGGCGACAACAGATACACAGATTT 987

Db 978 ACAGCTTCAGATGACACACAGTACTACAGATTTT 1010

Search completed: October 19, 2002, 23:33:08
Job time : 157.413 secs

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 Db 1309 ATACAAGTTACCCGAAACCCAGAGATGATTTTTTGGTAAACCCGAGAAATTCAGT 1250
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 Db 1249 ACTAGTATGATCTGTATGAGAAATTCCTCAATATATGTCACGACCTTACACGTT 1190
 Qy 601 TCTATCAGCTGTGCTCTCTCAGTCCCTGAGCAAGCAATGTGAGCATCTCTGTGCTCG 660
 Db 1189 TCTATCAGCTGTGCTCTCTCAGTCCCTGAGCAAGCAATGTGAGCATCTCTGTGCTCG 1130
 Qy 661 CAACCTGATGATTAACCTTCCCTCCTACCTTATATATAGATGACATTA 712
 Db 1129 CAACCTGATGATTAACCTTCCCTCCTACCTTATATATAGAAACCAACA 1078
 RESULT 15
 ID AAA49661
 AC AAA49661 standard; cDNA: 1050 BP.
 AC AAA49661;
 DT 25-SEP-2000 (first entry)
 XX Pig costimulatory molecule CD86 (B7-2) cDNA.
 DE Pig costimulatory molecule CD86 (B7-2) cDNA.
 XX Co-stimulatory molecule; CD86; B7-2; pig; immunosuppressive;
 KM xerotransplantation; organ transplant; vaccine; ss.
 OS Sus scrofa.
 OS
 FH Key Location/Qualifiers
 FT CDS 36..1013
 FT CDS /*tag= a
 XX W0200037102-A2.
 PN 29-JUN-2000.
 PD 17-DEC-1999; 99MO-GB04200.
 PF 19-DEC-1998; 98GB-0027921.
 PR 23-OCT-1999; 99GB-0025015.
 XX (MML-) ML LAB PLC.
 PA
 PI Lechler RI, Rogers NJ, Dorling A;
 PI WPI; 2000-442537/38.
 DR P-SDB; AAY95321.
 PT Novel methods for improving tolerance to a xenograft comprising
 PT immunizing a mammal with a T-cell epitope and a B-cell epitope -
 XX
 XX Disclosure: Fig 3; 81bp; English.
 XX
 XX The present sequence is that of cDNA clone CD86(1), which encodes
 CC pig co-stimulatory molecule CD86 (B7-2) (see AAY95321). The clone
 CC was obtained by PCR amplification of pig cDNA using primers (see
 CC AAA49662-63) based on a published pig B7-2 sequence. The invention
 CC relates to a novel strategy to inhibit costimulation by porcine
 CC cells of human T cells, with particular importance in the context
 CC of xerotransplantation of porcine organs. Recipients are immunised
 CC with hybrid synthetic peptides comprising a T cell epitope
 CC conjugated to sequences of the porcine costimulatory molecules
 CC CD80, CD86 or CD40. Peptides that induce antibodies specific for

CC regions of costimulatory molecules involved in binding to their
 CC counter-receptors on human cells (CD28 and CD14) are capable of
 CC blocking the delivery of costimulation. Once the antibody response
 CC has been induced, the transplanted organ will recall this response
 CC due to the expression of the costimulatory molecules, thereby
 CC sustaining the response, and providing an endogenous mechanism of
 CC costimulatory blockade. The method is useful for improving the
 CC tolerance of a host to xenografts, particularly porcine pancreatic
 CC islet cells.
 XX
 SQ Sequence 1050 BP; 305 A; 260 C; 227 G; 258 T; 0 other;
 Query Match 62.9%; Score 621; DB 21; Length 1050;
 Best Local Similarity 81.0%; Pred. No. 1e-176;
 Matches 804; Conservative 0; Mismatches 165; Indels 24; Gaps 6;
 Qy 10 AGATGACCTATGGAAGTGAATTAACATCTCTTGTGATGACCCCTGCTATAGTGTCT 69
 Db 27 AGTGGATCCATGGAGCTGAGTACATCTCTTGGGATGGTCTCTCTCTGTGTGCT 86
 Qy 70 GCTTCCATGAAGAGTCAAGCATATTTCAACAGAGCTGGAGACTGGCATTTTACA 129
 Db 87 GCCTCCTTGAAGAGTCAAGCATATTTCAACAGAGCTGGAGACTGGCATTTTACA 146
 Qy 130 AATTCTCAAAACATTAAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 189
 Db 147 AACTCGAGAACCTTAAGCCCTGATGATGATGATGATGATGATGATGATGATGATG 206
 Qy 190 GTTCTGACAGCTATTAACAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 249
 Db 207 GTTCTGACAGCTATTAACAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCAAG 266
 Qy 250 GGCCGCAAGAGCTTTGACAAAGCAATGAGCCCTGAGACTGATTAATTAATGAGATGAG 309
 Db 267 GGTGCGCAAGAGCTTTGACAAAGCAATGAGCCCTGAGACTGATTAATTAATGAGATGAG 326
 Qy 310 GACAAAGGCTTTGATCAATGATTTGTTGATCAATTAAGAGGAGGAGGAGGAGGAGG 369
 Db 327 GACAAAGGCTTTGATCAATGATTTGTTGATCAATTAAGAGGAGGAGGAGGAGGAGG 386
 Qy 370 CACCAGATGAATTCGACCATTAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 429
 Db 387 CACCAGATGAATTCGACCATTAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 446
 Qy 430 ACTTCTAATAGAAACAAAATTTGAGCATCAATTAATTTGAGCTGCTGCTGCTGCTGCTG 489
 Db 447 CTACTAATACACAGAAATTTCTG---TCATAAATTGAGCTGCTGCTGCTGCTGCTGCTG 503
 Qy 490 TACCCGAAACCCAGAGAGATGATTTTGGTAAACCCGAGAAATTAATTAATTAATTAAT 549
 Db 504 TACCCGAAACCCAGAGAGATGATTTTGGTAAACCCGAGAAATTAATTAATTAATTAAT 563
 Qy 550 GATACGTGATGAAGAAATTCATAAATATATGACAGAACTGTACAGGTTCTCTGACG 609
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 Qy 610 TTGCTCTTCGAGCTCCGTAAGCAAGCAATGAGCATCTTCTGCTGCTGCTGCTGCTGCTG 669
 Db 624 GTGCTCTTCGAGCTCCGTAAGCAAGCAATGAGCATCTTCTGCTGCTGCTGCTGCTGCTG 683
 Qy 670 TCAATGAA-----GCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 684 CCAAGCAACACTCTCTTCTCCCTACCTGTTATATAGATGAACCAACCTGCTGCTGCTG 743
 Qy 721 ACCCTGATGAGAGCACATCTCTGATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 744 CCCCTGATGAGAGCACATCTCTGATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803
 Qy 781 TGTGGAGTGTGTTCTTCTTAACACTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 804 TGTGGAGTGTGTTCTTCTTGAACACTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
 Qy 841 CATGAT---GTGAACCAACAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897

XX
AC AA727922.

Db 1489 CAGATCAAGGACAAGGCGTTGTATCAATGTTTCGTTCAATCAATAAGGCCCCAAAGGACTC 1430

XX
AC AA227922;

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Db 541 ACTAAGTATGATACGTGCATGGAAGAAATCTCAAAATATGTCACAGACTCTACAGCTT 600
QY 601 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAGCAAGCATGTGAGCATCTTCTGTGCTG 660
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Db 601 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAGCAAGCATGTGAGCATCTTCTGTGCTG 660
QY 661 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATGATGACACATA 712
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Db 661 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATGAAACCAACA 712

RESULT 12
AA227924/C
ID AA227924 standard; DNA; 840 BP.
XX
XX AA227924;
AC
XX
XX 20-DEC-1999 (first entry)
DT
XX
DE Complementary strand of canine B7-2S coding sequence.
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
OS
XX
XX WO9947558-A2.
PN
XX
XX 23-SEP-1999.
PD
XX
XX 19-MAR-1999; 99WO-US06187.
PE
XX
XX 19-MAR-1998; 98US-0078765.
PR
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX PA
XX
XX PI Sim G, Yang S, Sellins KS.
XX
XX WPI; 1999-571822/48.
DR
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX PS Claim 1; Page 115; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
XX SQ Sequence 840 BP; 214 A; 167 C; 181 G; 278 T; 0 other;

Query Match 71.3%; Score 704; DB 20; Length 840;
Best Local Similarity 99.3%; Pred. No. 8.6e-202;
Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGTATCTCAGATGCACTATGAGACTGAATAACATTCCTTTGTGATGACCCCTCGCTC 60
    |||
Db 840 ATGTATCTCAGATGCACTATGAGACTGAATAACATTCCTTTGTGATGACCCCTCGCTC 781
QY 61 TATGGTGGCTTCATGCAAGAGTCAAGCATTTTCAACAAGACGCGAGACTGCGCATGC 120
    |||
Db 780 TATGGTGGCTTCATGCAAGAGTCAAGCATTTTCAACAAGACGCGAGACTGCGCATGC 721
QY 121 CATTTTACAATTTCTCAAAACATAGCCTGATGAGTGTGTGTTTGGCAGGACGAG 180
    |||

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Db 720 CATTTTACAATTTCTCAAAACATAGCCTGGATGAGTTGTAGTGTGTTGGCAGGACGAG 661
QY 181 GATAAGCTGTTCTGTGTAGAGCTATACAGAGCAAGAAACCCCTCAAAATGTTTCATCGC 240
    |||
Db 660 GATAAGCTGTTCTGTGTAGAGCTATACAGAGCAAGAAACCCCTCAAAATGTTTCATCGC 601
QY 241 AAGTATTAAGGGCCGACACAGCTTTGACAAAGACAAATTTGAGACCCCTGAGACTCCATTAATTT 300
    |||
Db 600 AAGTATTAAGGGCCGACACAGCTTTGACAAAGACAAATTTGAGACCCCTGAGACTCCATTAATTT 541
QY 301 CAGATCAAGCAAGAGGCGCTTATCAATGTTTCTGTCATCATCAATAAAGGCCCAAGGACTC 360
    |||
Db 540 CAGATCAAGCAAGAGGCGCTTATCAATGTTTCTGTCATCATCAATAAAGGCCCAAGGACTC 481
QY 361 GTTCCCATGACACCAAGATGAATTCAGCTATCAGTGTGCTTAACCTCAGTCAACCTGAA 420
    |||
Db 480 GTTCCCATGACACCAAGATGAATTCAGCTATCAGTGTGCTTAACCTCAGTCAACCTGAA 421
QY 421 ATATGTTAAGTCTCTAATAGAACAGAAAATTCGAGCATCATTAATTTGACCTGCTCATTC 480
    |||
Db 420 ATATGTTAAGTCTCTAATAGAACAGAAAATTCGAGCATCATTAATTTGACCTGCTCATTC 361
QY 481 ATACAAGGTTACCCAGAAACCCAGAGAGATGATTTTGGTAAACCCGAGAAATTCAGT 540
    |||
Db 360 ATACAAGGTTACCCAGAAACCCAGAGAGATGATTTTGGTAAACCCGAGAAATTCAGT 301
QY 541 ACTAAGTATGATGACTGTCATGAGAAATCTCAAAATATATGTCACAGAACTTACACGTT 600
    |||
Db 300 ACTAAGTATGATGACTGTCATGAGAAATCTCAAAATATATGTCACAGAACTTACACGTT 241
QY 601 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGCTG 660
    |||
Db 240 TCTATCAGCTTGTCTCTCTCAGTCCCTGAAGCAAGCAATGTGAGCATCTTCTGTGCTG 181
QY 661 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATAGAACCAACA 712
    |||
Db 180 CAACCTGAGTCATGAAGCTTCCCTCCCTACCTTATATATAGAACCAACA 129

RESULT 13
AA227921
ID AA227921 standard; DNA; 1795 BP.
XX
XX AA227921;
AC
XX
XX 20-DEC-1999 (first entry)
DT
XX
XX Canine B7-2S protein encoding DNA.
DE
XX
XX B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
OS
XX
XX WO9947558-A2.
PN
XX
XX 23-SEP-1999.
PD
XX
XX 19-MAR-1999; 99WO-US06187.
PE
XX
XX 19-MAR-1998; 98US-0078765.
PR
XX 17-APR-1998; 98US-0062597.
XX
XX (HESK-) HESKA CORP.
XX
XX PA
XX
XX PI Sim G, Yang S, Sellins KS.
XX
XX WPI; 1999-571822/48.
DR
XX P-PSDB; AAY41078.
DR
XX
XX New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases

```

Db 259 TGTATGAGATATTTCAGAGCCAAAGAACCTCAAAATGTTTCATCTCAATATTAAGGCC 318
QY 254 GCACAGCTTTGCAAGAACAAFTTGACCTGAGACTCCATATATPTGATGATCAAGAGCA 313
Db 319 GTACAAAGCTTTGCAAGAACAAFTTGACCTGAGACTCCATATATPTGATGATCAAGAGCA 378
QY 314 AGGGCTTGTATCAATGTTTCGTTTCATCATTAAGAGGCCCAAGAGCTGTTCCCATGACCC 373
Db 379 AGGGCAATATCACTGTTTCATTCATATTAAGAGGCCCAAGAGCTGTTCCCATGACCC 438
QY 374 AGATGATTTCTGACATATGATGCTTGTCTTACTTCACTCACTCACTCACTCACTCACT 433
Db 439 AATGAGTTCTGACATATGATGCTTGTCTTACTTCACTCACTCACTCACTCACTCACT 498
QY 434 CTATATGACAGAAATTTGTCATCATTAATTTGACCTGCTCACTCACTCACTCACTCACT 493
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QY 494 CAGAACCCAGAGATATTTTGTGTAAACCGAGATTTCAAGTACTATAGATATAT 553
Db 559 CAGAACCTTAAGAGATATTTTGTGTAAACCGAGATTTCAAGTACTATAGATATAT 618
QY 554 CTGTCTATGAAGAAATCTCAAAATATGTACAGAACTCTACAGCTTTTCTATCAGCTTGT 613
Db 619 CTGTCTATGAAGAAATCTCAAAATATGTACAGAACTCTACAGCTTTTCTATCAGCTTGT 678
QY 614 CTTTCTCAGTCCCTGAGAGCAATGTGACATCTTCTGTGCTGCACTGAGTCA 673
Db 679 CTTTCTCAGTCCCTGAGAGCAATGTGACATCTTCTGTGCTGCACTGAGTCA 738
QY 674 T---GAAGCTTCCCTCCCTTACTTATATATAGATGACACA---TACGAAACCCACCCCTG 727
Db 739 TGGAGATGCTGCTCTCCCTTCAATATATAGATGACACAACCTTAAGATTAAGACCTG 798
QY 728 ATGAGACACATCTCTGATTTGGGGCTGCTGTTTATATGTTGTCATTTTGTGGGA 787
Db 799 AACAGGCCCACTTCTCTGATTTGGGGCTGCTGTTTATATGTTTGTGGGA 858
QY 788 TGGTGTCTTTCTTCACTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
Db 859 TGGTGTCTTTTAAACACTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
QY 848 GTGAAACCAACAAAGTGAG 907
Db 919 GTGAAACCAACAAAGTGAG 978
QY 908 ATGAAAGGAAAGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 967
Db 979 AGCTACCTGAGAGATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
QY 968 ACAACAGT 975
Db 1039 ACAAAT 1046

RESULT 11
AAZ27923
ID AAZ27923 standard; DNA; 840 BP.
XX
XX AAZ27923:
AC
XX
XX 20-DEC-1999 (first entry)
XX
XX Canine B7-25 protein coding sequence.
DE
XX
XX B7: CTLA4: T cell costimulatory protein; dog; cat: autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX Canis familiaris.
OS
XX
XX WO947558-A2.
PN

PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99WO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
DR P-PSDB: AAY41078.
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
XX
XX
PS Claim 1; Page 114; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 840 BP; 278 A; 181 C; 167 G; 214 T; 0 other;
XX
XX
XX Query Match 71.3%; Score 704; DB 20; Length 840;
XX Best Local Similarity 99.3%; Pred. No. 8.e-202;
XX Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGTATCTCAATGACATGAGTGAATCAATCTCTTGTGATGAGACCTCTGCTC 60
Db 1 ATGTATCTCAATGACATGAGTGAATCAATCTCTTGTGATGAGACCTCTGCTC 60
QY 61 TATGCTGCTGCTTCATGAGAGTCAAGCATATTTCAACAAGAGTGAAGTCCATGTC 120
Db 61 TATGCTGCTGCTTCATGAGAGTCAAGCATATTTCAACAAGAGTGAAGTCCATGTC 120
QY 121 CATTTTACAAATTTCTCAAAACATAGAGCTGATGATGTTGTGTTGGCAGGACAG 180
Db 121 CATTTTACAAATTTCTCAAAACATAGAGCTGATGATGTTGTGTTGGCAGGACAG 180
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Db 181 GATAGCTGCTTCTGTAGAGCTATACAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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Db 301 CAGATCAAG 360
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QY 541 ACTAGTATGATGCTGATGAG 600
Db 541 ACTAGTATGATGCTGATGAG 600


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Db 2576 CCATGAAAGCAAGCAACATATTTCAACAAGACTGGAGAACTGCCATTATTTCAAACT 2517
Oy 134 CTCAAAACATAGAGCTGGATGAGTTGTAAGTTTGGCAGAGCAGATTAAGCTGTTC 193
Db 2516 CTCAAAACATAGAGCTGGATGAGTTGTAAGTTTGGCAGAGCAGATTAAGCTGTTC 2457
Oy 194 TGTACGACTATACAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAGTATAGGGCC 253
Db 2456 TGTATGATATATTCAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAGTATAGGGCC 2397
Oy 254 GCACAAGCTTTGACAAACAAATGGACCCGAGACCTCATTAATATGATCAAGACA 313
Db 2396 GTACAAAGCTTTGACAAAGCAACTGGACCTGAGCTCCACAAATGTTTCAGTCAAGACA 2337
Oy 314 AGGCTTATATCAATGTTTCTCATCAATAAGGCCCAAGAGACTGCTCCATGCAAC 373
Db 2336 AGGCAACATATCACTGTTTCATTCATTAAGGGCCCAAGAGACTGCTCCATGCAAC 2277
Oy 374 AGATGAATTCGACTATACAGTGTGCTGTAACCTCAGTCAACCTGAATATGTAACCT 433
Db 2276 AATAGGTTCTGACCTATCAAGTGTGCTGTAACCTCAGTCAACCTGAATATGTAACCT 2217
Oy 434 CTAATAGAACAAATTTCTGCAATCAATAATTTGACCTGCTCATCCATACAGGTTAC 493
Db 2216 CTAATAGAACAAATTTCTGCAATCAATAATTTGACCTGCTCATCCATACAGGTTAC 2157
Oy 494 CAGAACCCAGAGAGATGATTTTTTGTAAAAACCGAGAAATTCAGTCAAGTATGATA 553
Db 2156 CAGAACCTAAGAGAGATGATTTTTTGTAAAAACCGAGAAATTCAGTCAAGTATGATA 2097
Oy 554 CAGTATAGAGAAATCTCAAAATATGTCAGCAAGCTACAGCTTCTATCAGCTTGT 613
Db 2096 CAGTATAGAGAAATCTCAAAATATGTCAGCAAGCTACAGCTTCTATCAGCTTGT 2037
Oy 614 CCTTCAGTCCCTGAGCAAGCAATGTGAGCATCTTGTCTCTGCACTTGAGTCA 673
Db 2036 CTTTTCAGTCCCTGAGCAAGCAATGTGAGCATCTTGTCTCTGCACTTGAGTCA 1977
Oy 674 T---GAAGTTCCTCCCTACCTTATATATGATGACACA---TACGAACCCACCCCTG 727
Db 1976 TGGAGATGCTGCTCTCCCTACCTTCAATATATGATGACACAACCTAAGGTAAGACCTG 1917
Oy 728 ATGAGAACACATCTCTGATTTGGGCTCTGCTGTATGTTGGTCAATTTTGTGGGA 787
Db 1916 AACAGGCCACTCTCTGATTTGGGCTCTGCTGTATGTTGGTCAATTTTGTGGGA 1857
Oy 788 TGGTGTCTTCTTACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
Db 1856 TGGTGTCTTCTTAAACACTAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797
Oy 848 GTGAAGCAACAAAGTGGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
Db 1796 GTGAAGCAACAAAGTGGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
Oy 908 ATGAAGAGAGAAAGATCTGATGAAGCCAGTGTGTTAACATTTTGAAGAGAGAGAGAG 967
Db 1736 AGCTACTCTGAGAGATCTGATGAAGCCAGTGTATTAACATTTTGAAGAGAGAGAGAG 1677
Oy 968 ACAACGTAATACAGAGTTT 987
Db 1676 ACAAAAGTAATACAGAGTTT 1657

```

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XX CD86; B7-2; feline; cat; recombinant virus; vaccine;
KW Immunomodulator; tumour; cancer; therapy; ss.
XX Fells domesticus.
OS Key Location/Qualifiers
FH CDS 63..1052
FT /tag= a
FT MO957295-A1.
XX 11-NOV-1999.
XX 30-APR-1999; 99MO-US09504.
XX 01-MAY-1998; 98US-0071711.
XX (SCHE ) SCHERING-PLOUGH LTD.
PA (SCHE ) SCHERING-PLOUGH VETERINARY CORP.
XX Winslow BJ, Cochran MD;
XX MPI: 2000-062155/05.
XX P-SDB: AAY32285.
XX Novel recombinant virus useful as immunomodulators, particularly in
PT vaccines -
XX Disclosure; Fig 3a; 230pp; English.
XX This is the nucleotide sequence of cDNA coding for feline CD86
CC (B7-2). The cDNA was isolated from feline peripheral blood
CC mononuclear cell cDNA by PCR. Manipulating the expression of CD28
CC or CTLA-4 (and/or their co-stimulatory ligands CD80 and CD86)
CC regulates T cell proliferation and cytokine release. The invention
CC relates to a recombinant virus that contains at least one foreign
CC nucleic acid, inserted into a nonessential genomic region, that
CC encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their
CC immunogenic fragments, and is expressed when the recombinant virus
CC is introduced into a suitable host. The invention also provides:
CC a recombinant virus further comprising a foreign nucleic acid
CC encoding an immunogen derived from a feline pathogen; recombinant
CC viruses capable of enhancing an immune response to protect against
CC disease; recombinant viruses expressing antisense sequences,
CC capable of suppressing an immune response in a feline, e.g., for
CC treatment of autoimmune disease or transplant rejection; and
CC recombinant viruses expressing DNA encoding CD80 and/or CD86 used
CC to reduce or eliminate a tumour in cats.
XX
SQ Sequence 1080 BP; 333 A; 233 C; 235 G; 279 T; 0 other;
Query Match 78.3%; Score 772.8; DB 21; Length 1080;
Best Local Similarity 88.8%; Pred. No. 1,8e-222;
Matches 860; Conservative 0; Mismatches 102; Indels 6; Gaps 2;
Oy 14 GCATATGAGAACTGAATACATCTCTTGTGATGACCTCTGCTATAGTGCTCTT 73
Db 79 GCATATGAGAACTGAATACATCTCTTGTGATGAGCCCTCTGCTCTGCTCTTCTT 138
Oy 74 CCATGAAGAGCAAGCATATTTCAACAAAGAGTGGAGAGAGAGAGAGAGAGAGAGAG 133
Db 139 CCATGAAGAGCAAGCATATTTCAACAAAGAGTGGAGAGAGAGAGAGAGAGAGAGAG 198
Oy 134 CTCAAAACATAGAGCTGGATGAGTTGTAAGTTTGGCAGAGCAGATTAAGCTGTTC 193
Db 199 CTCAAAACATAGAGCTGGATGAGTTGTAAGTTTGGCAGAGCAGATTAAGCTGTTC 258
Oy 194 TGTACGACTATACAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAGTATAGGGCC 253
Db 259 TGTATGATATATTCAGAGGCAAGAAACCTCAAAATGTTTCATCGCAAGTATAGGGCC 318
Oy 254 GCACAAGCTTTGACAAACAAATGGACCTGAGACCTCATTAATATGATCAAGACA 313

```

PT treating, e.g. autoimmune and atopic diseases -
 XX
 PS Claim 1; Page 116-119; 148pp; English.
 XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 2830 BP; 877 A; 570 C; 586 G; 797 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 2830;
 Best Local Similarity 89.0%; Pred. No. 7e-226;
 Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATGAGTGAATACATCTCTTTGATGACCCCTGCTATAGTGTGCTT 73
 DB 195 GCACATGAGTGAATACATCTCTTTGATGACCCCTGCTATAGTGTGCTT 254
 QY 74 CCATGAAGAGTCAAGCATATTTCAACAAGAGTGAAGAGTGCATTTTACAAT 133
 DB 255 CCATGAAGAGTCAAGCATATTTCAACAAGAGTGAAGAGTGCATTTTACAAT 314
 QY 134 CTCAAAACATAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 193
 DB 315 CTCAAAACATAGCTGTGATGATGATGATGATGATGATGATGATGATGATG 374
 QY 194 TGTACGAGCTATACAGGAGCAAGAAACCTCAAAATGTTTCATCGCATATTAAGGCC 253
 DB 375 TGTATGAGATATTTACAGAGCAAGAAACCTCAAAATGTTTCATCGCATATTAAGGCC 434
 QY 254 GCACAAGCTTTGACAAAGACATTTGGACCTGACATTCATATTTCAATCAAGACA 313
 DB 435 GTACAAGCTTTGACAAAGACATTTGGACCTGACATTCATATTTCAATCAAGACA 494
 QY 314 AGGGCTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 373
 DB 495 AGGGCAATATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 554
 QY 374 AGATGAATTTGACATTCATGATGATGATGATGATGATGATGATGATGATG 433
 DB 555 AATGATGATTTGACATTCATGATGATGATGATGATGATGATGATGATGATG 614
 QY 434 CTAATGAAGCAAAATTTCTGCATCATTAATTTGACCTGCTCATCTATACAGTTACC 493
 DB 615 CTAATGAAGCAAAATTTCTGCATCATTAATTTGACCTGCTCATCTATACAGTTACC 674
 QY 494 CAGAACCCAGAGATGATTTTGTAAACCGAGATTTCAAGTACTAGATGATA 553
 DB 675 CAGAACCCAGAGATGATTTTGTAAACCGAGATTTCAAGTACTAGATGATA 724
 QY 554 CCGTATGAAGAAATCTAAATATGACAGAACTCAACGTTTATCAAGCTGT 613
 DB 725 CCGTATGAAGAAATCTAAATATGACAGAACTCAACGTTTATCAAGCTGT 794
 QY 614 CTTTCAAGCTGTCGACAAAGCAAGATGATGATGATGATGATGATGATGATG 673
 DB 795 CTTTCAAGCTGTCGACAAAGCAAGATGATGATGATGATGATGATGATGATG 854
 QY 674 T---GAAGCTTCCCTACCTATATATATGATGACA---TACGAACCCACCCCTG 727
 DB 855 TGAAGATGCTGCTCCCTACCTATATATATGATGACAACCAAGATTAAGACCTG 914
 QY 728 ATGAGAGACACATCTCTGATGATGATGATGATGATGATGATGATGATGATG 787
 DB 915 AACAGAGCCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 974
 QY 788 TGGTGTCT 847

DB 975 TGGTGTCT 1034
 QY 848 GTGAACCCAGAGATGATTTTGTAAACCGAGATTTCAAGTACTAGATGATA 907
 DB 1035 GTGAACCCAGAGATGATTTTGTAAACCGAGATTTCAAGTACTAGATGATA 1094
 QY 908 ATGAAGCCGAAAGATCTGATGATGATGATGATGATGATGATGATGATGATG 967
 DB 1095 ACCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1154
 QY 968 ACAACAGTACTACAGATTT 987
 DB 1155 ACAACAGTACTACAGATTT 1174

RESULT 8
 AA227930/C
 ID AA227930 standard; DNA; 2830 BP.
 XX
 NC AA227930;
 DT 20-DEC-1999 (first entry)
 XX
 DE Feline B7-2 gene complementary DNA sequence.
 XX
 KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
 KW allergic reaction; infectious disease; tumor development; feline;
 KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
 XX
 OS Fells catus.
 XX
 PN W09947558-A2.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99MO-US06187.
 XX
 PR 19-MAR-1998; 98US-0078765.
 PR 17-APR-1998; 98US-0062597.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Sellins KS;
 DR WPI; 1999-571822/48.
 XX
 PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
 PT treating, e.g. autoimmune and atopic diseases -
 XX
 PS Claim 1; Page 121-123; 148pp; English.

XX
 CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
 CC encoding nucleic acid molecules from dogs and cats. The proteins can be
 CC expressed by standard recombinant methodology. The nucleic acid molecules
 CC and the encoded proteins can be used for preventing or treating diseases,
 CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
 CC development, graft rejection, inflammation, arthritis and atopic diseases
 CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
 CC cats, cattle, sheep or pets. The products can also be used for detection,
 CC diagnosis and drug screening.
 XX
 SQ Sequence 2830 BP; 797 A; 586 C; 570 G; 877 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 2830;
 Best Local Similarity 89.0%; Pred. No. 7e-226;
 Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATGAGTGAATACATCTCTTTGATGACCCCTGCTATAGTGTGCTT 73
 DB 2636 GCACATGAGTGAATACATCTCTTTGATGACCCCTGCTATAGTGTGCTT 2577
 QY 74 CCATGAAGAGTCAAGCATATTTCAACAAGAGTGAAGAGTGCATTTTACAAT 133

DE	Complementary strand of feline B7-2 coding sequence.
xx	
KW	B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KM	allergic reaction; infectious disease; tumor development; feline;
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.
xx	
OS	Felis catus.
xx	
PN	W09947558-A2.
xx	
PD	23-SEP-1999.
xx	
PF	19-MAR-1999; 99WO-US06187.
xx	
PR	19-MAR-1998; 98US-0078765.
FR	17-APR-1998; 98US-0062597.
xx	
PA	(HESK-) HESKA CORP.
xx	
PI	Slim G, Yang S, Sellins KS;
xx	
DR	WPI: 1999-571822/48.
xx	
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for
xx	treating, e.g., autoimmune and atopic diseases -
xx	
PS	Claim 1; Page 124-125; 148pp; English.
xx	
CC	The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC	encoding nucleic acid molecules from dogs and cats. The proteins can be
CC	expressed by standard recombinant methodology. The nucleic acid molecules
CC	and the encoded proteins can be used for preventing or treating diseases,
CC	e.g., autoimmune diseases, allergic reactions, infectious diseases, tumor
CC	development, graft rejection, inflammation, arthritic and atopic diseases
CC	such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC	cats, cattle, sheep or pets. The products can also be used for detection,
CC	diagnosis and drug screening.
xx	
SQ	Sequence 996 BP; 255 A; 203 C; 219 G; 319 T; 0 other;
	Query Match 79.5%; Score 784.8; DB 20; Length 996;
	Best Local Similarity 89.0%; Pred No. 4.1e-226;
	Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2
OY	14 GCACATGAGACTGATAACATCTCTTTGTGATGACACCCTCGCTCATAGTGTCCTT 73
Dd	
	980 GCACATGAGACTGATGCACACTCCTCTGTGATGGCCCTCGCTCTGTGGTTTTCTT 921
OY	74 CCATGAAGCTCAACGATATTTCACAAAGACTGGAGAATGCCATGCCATTTTACAATT 133
Dd	
	920 CCATGAAGAGTCAAGCATTTTTCACAAAGCGAGAACATGCCATGCCATTTTACAACCT 861
OY	134 CTCAAAACCTTAAGCCCTGATGTGATGGTGGTCTTTTGGAGAGCACGATTAAGCTGTTTC 193
Dd	860 CTCAAAACCTTAAGCCCGATGTGAGCTGTGTATTTTGGCAGGACCGATTAAGCTGTTC 801
OY	194 TGTAGAGCTATACAGAGCCAAAGAGACCCCTCAAATTTTCATGCGCAAGTAAAGGCC 253
Dd	
	800 TGTATGAGTATTTTCAGAGCCAAAGAGAACCCCTCAAATTTTCATCTCCAATTAAGGGCC 741
OY	254 GGACAAAGCTTTGACAAAGCAATTTGGACCCCTGAGACTCCATTAATTTTCAGATCAAGGACA 313
Dd	740 GTTACAAAGCTTTGACAAAGCAATTTGGACCCCTGAGACTCCACATTTTTCAGATCAAGGACA 681
OY	314 AGGGCTTGATCAATGTTTGTCATCATTAAGGGCCAAAGAGCTGTTCCCATGCAACC 373
Dd	680 AGGGCCATATCACTGTTTCATTCATTATAAAGGGCCCAAAGAGCTATCCCATGCACC 621
OY	374 AGAGTAAATTTCTGACCAATAGAGCTTGGCAATCTGATCAACCTGAAATAAATAGTAACTT 433
Dd	620 AAATGAGTTCTGACCAATATGAGCTTGGCTTCACTTCACTGATCAACCTGAAATAAATAGTAACTT 561
OY	434 CTAAATGAACAGAAAAATTCCTGGATCATTAATTTGAACCTGCTCATCCATCAAGGTTAAC 493

Db	560	CTAATAGACGAGAAATTCGTGGCATTCATTAATTTGGACCTGCTCATCATACAGGTTACC	501
QY	494	CAGAACCCAGAGATGTATTTTTTGGTAAAAAOCGGAATTCAGTACTAAGTATGATA	553
Db	500	CAGAACCTAAGAGATGTATTTTTCAGCTAAACACTGAGATTCAGTACTAAGTATGATA	441
QY	554	CTGTGCATGANAATATCTCAAAATTAATGTCCACAGACACTCCAAACGTTTCTATCAGCTTG	613
Db	440	CTGTGCATGANAATATCTCAAAATTAATGTGTGACAGACTGTCAACGTTTCTATCAGCTTG	381
QY	614	CTTTCTCAGTCCCTGGAAGCAAGCAATGTGAGCATCTTCTGTCTCCGCAACTGAGTCAA	673
Db	380	CTTTTTCAGTCCCTGGAAGCAACATGTGAGCGTCTTTGTGGCCCTGAAACTGAGACAC	321
QY	674	T---GAGCTTCCCTCCCTACCTTATATATAGTGCACA---TAGAAGAACCAACCCCTG	727
Db	320	TGGAGATGCTCCTCTCTCCCTACCTTTCATATATAGTGCACAACCTTAAGATTAAGACCCCTG	261
QY	728	ATGGAAGCAACATCCTCGATTCGAGTTCCGGCTCGCTGTGAATGTTGGTATTTGTGGGA	787
Db	260	AACAGAGCCACTTCTCTCTGGAATTCGGGCTGTACTTGAATGTTGTGTTTGTGGGA	201
QY	788	TGTGTGTTCTTCTTCAACACTAAGAAGAAAGAAAGAGACAGCCTGGCCCTCTCATGAT	847
Db	200	TGTGTGTTCTTCTTAAACACTAGAGAAAGAAAGAGACAGCCTGGCCCTCTCATGAT	141
QY	848	GTGAACCCACAAAGTGGAGAGAAAAGAAAGTGAAGACACCAAGAAAGTACGGTACC	907
Db	140	GTGAACCCATCAAAAAGGAGAGAAAGAGACCAACAGACCAAGAAAGTACCATACC	81
QY	908	ATGAAGCCGAAAGATCTGATAGAGCCCGACAGTGTGTTAACTTTCCAGACAGCTTCAGGC	967
Db	80	ACGTACCTGAGAGATCTGATAGAGCCCGACAGTGTATTAACTTTGAAGACAGCCTCAGGC	21
QY	968	ACAACAGTACTACACAGTTT 987	
Db	20	ACAAAAGTACTACACATTTT 1	
RESULT 7			
AAZ27929			
ID	AAZ27929 standard; DNA; 2830 BP.		
XX			
AC	AAZ27929;		
XX			
DT	20-DEC-1999 (first entry)		
XX			
DE	Feline B7-2 protein encoding DNA.		
XX			
B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune diseases			
KW	allergic reaction; infectious disease; tumor development; feline;		
KM	graft rejection; inflammation; arthritis; atopic dermatitis; ss.		
XX			
OS	Felis catus.		
XX			
PN	W09947558-A2.		
XX			
PD	23-SEP-1999.		
XX			
PF	19-MAR-1999; 99WO-US06187.		
XX			
PR	19-MAR-1998; 98US-0078765.		
PR	17-APR-1998; 98US-0062597.		
XX			
PA	(HESK-) HESKA CORP.		
XX			
PI	Slim G, Yang S, Sellins KS;		
XX			
DR	WPI; 1999-571822/48.		
XX			
DR	P-PSDB; AAY41079.		
XX			
PT	New isolated B7 and CTLA4 nucleic acids, used to develop products for		

Db 1112 TGTGGATGTCTTCTTCTACACTAAGGAAGGAAGAAACAGCCGCGCCCTCT 1053
QY 841 CATTGATGTGAACCAACAAAGTGGAGAAAGAAAGTGAAGCAACAGAAAGAGTA 900
Db 1052 CATTGATGTGAACCAACAAAGTGGAGAAAGAAAGTGAAGCAACAGAAAGAGTA 993
QY 901 CGGTACCATGAAGCGAAAGATCTGATGAGCCAGTGTGTTAACATTTCGAAGCAGCT 960
Db 992 CGGTACCATGAAGCGAAAGATCTGATGAGCCAGTGTGTTAACATTTCGAAGCAGCT 933
QY 961 TCAGCGGACACAGTACTACACAGTTT 987
Db 932 TCAGCGGACACAGTACTACACAGTTT 906

RESULT 5

AA227931
ID AA227931 standard; DNA; 996 BP.

AA227931;

20-DEC-1999 (first entry)

Feline B7-2 protein coding sequence.

B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

allergic reaction; infectious disease; tumor development; feline;

graft rejection; inflammation; arthritis; atopic dermatitis; ss.

Felis catus.

W09947558-A2.

23-SEP-1999.

19-MAR-1999; 99WO-US06187.

19-MAR-1998; 98US-0078765.

17-APR-1998; 98US-0062597.

(HESK-) HESKA CORP.

WPI: 1999-571822/48.

P-PSDB: AAY41079.

Slm G, Yang S, Sellins KS;

New isolated B7 and CTLA4 nucleic acids, used to develop products for

treating, e.g. autoimmune and atopic diseases

Claim 1: Page 123-124; 148bp; English.

The invention provides B7 and CTLA4 (T cell costimulatory proteins)

encoding nucleic acid molecules from dogs and cats. The proteins can be

expressed by standard recombinant methodology. The nucleic acid molecules

and the encoded proteins can be used for preventing or treating diseases,

e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor

development, graft rejection, inflammation, arthritis and atopic diseases

such as atopic dermatitis. They can be used in mammals such humans, dogs,

cats, cattle, sheep or pets. The products can also be used for detection,

diagnosis and drug screening.

Sequence 996 BP; 319 A; 219 C; 203 G; 255 T; 0 other;

Query Match 79.5%; Score 784.8; DB 20; Length 996;

Best Local Similarity 89.0%; Pred. No. 4.1e-226;

Matches 872; Conservative 0; Mismatches 102; Indels 6; Gaps 2;

QY 14 GCACATATGGAAGTGAATACATCTCTTTGTGATGAGCCCTGCTCTATGATGCTGCTT 73
Db 17 GCACATATGGAAGTGAATACATCTCTCTGTATGAGCCCTGCTCTGCTGCTGCTTCTT 76

QY 74 CCATGAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGCTATTTACAATT 133
Db 77 CCATGAGAGTCAAGCATATTTTCAACAAGACTGGAGAACTGCCATGCTATTTACAAC 136
QY 134 CTCAAAACATTAAGCCTGGATGAGTGTGATGTTTGGCAGGACCAAGATAGCTGTTG 193
Db 137 CTCAAAACATTAAGCCTGGATGAGTGTGATGTTTGGCAGGACCAAGATAGCTGTTG 196
QY 194 TGTACGACTATACAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 253
Db 197 TGTATGATATATTCAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 256
QY 254 GCACACCTTTGACAAAGACAATTTGGACCTGGAGCTCCATATATTCAGATCAAGGACA 313
Db 257 GTACAGCTTTGACAAAGACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 316
QY 314 AGGCTTGTATCAATGTTTGTTCATCATTAAGGCGCAAGGACGCTGCTCCATGACC 373
Db 317 AGGCAATATACACTGTTTATTCATCATTAAGGCGCAAGGACGCTGCTCCATGACC 376
QY 374 AGATGAATTTCTGACCTATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
Db 377 AATGAGTTTCTGACCTATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
QY 434 CTATATGACAGAAATTTTGGCATCATTAATTTGACCTGCTGCTGCTGCTGCTGCTGCT 493
Db 437 CTATATGACAGAAATTTTGGCATCATTAATTTGACCTGCTGCTGCTGCTGCTGCTGCT 496
QY 494 CAGAACCAAGAGATGATTTTGTGTAACCAAGCAAGCAAGCAAGCAAGCAAGCAAG 553
Db 497 CAGAACCAAGAGATGATTTTGTGTAACCAAGCAAGCAAGCAAGCAAGCAAGCAAG 556
QY 554 CTGTCATGAAGAAATCTCAAAATATGTCAGCAAGCAAGCAAGCAAGCAAGCAAGCA 613
Db 557 CTGTCATGAAGAAATCTCAAAATATGTCAGCAAGCAAGCAAGCAAGCAAGCAAGCA 616
QY 614 CTTTTCAGTCCCTGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 673
Db 617 CTTTTCAGTCCCTGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 676
QY 674 T---GAAGCTTCCCTGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 727
Db 677 TGAAGATGCTGCTCCCTGGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 736
QY 728 ATGAGACCAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 787
Db 737 AACAAGCCACTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 796
QY 788 TGTGTTCTTTTCAACATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 847
Db 797 TGTGTTCTTTTCAACATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 856
QY 848 GTGAACCAACAAAGTGGAGAGAAAGAAAGTGAAGCAAGCAAGCAAGCAAGCAAG 907
Db 857 GTGAACCAACAAAGTGGAGAGAAAGAAAGTGAAGCAAGCAAGCAAGCAAGCAAGCA 916
QY 908 ATGAACCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 967
Db 917 AGCTACTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 976
QY 968 ACAACAGTACTACACAGTTT 987
Db 977 ACAAAAGTACTACACAGTTT 996

RESULT 6

AA227932/c

ID AA227932 standard; DNA; 996 BP.

AA227932;

20-DEC-1999 (first entry)

```
OY 421 ATAAATGTAAGTCTTAATAGACAGAAAAATTCGTGCATCATTAATTTGACCTGCTCATCC 480
    |||
DB 426 ATAAATGTAAGTCTTAATAGACAGAAAAATTCGTGCATCATTAATTTGACCTGCTCATCC 485
OY 481 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGGTAAAAAACCGAGAATTCAGAT 540
    |||
DB 486 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGGTAAAAAACCGAGAATTCAGAT 545
OY 541 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATATATGTCACGAACTCTACAACTT 600
    |||
DB 546 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATATATGTCACGAACTCTACAACTT 605
OY 601 TCTATCAGCTTGTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCTCTG 660
    |||
DB 606 TCTATCAGCTTGTCTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCTCTG 665
OY 661 CAACCTTGACTCAATGAAAGCTTCCCTCCCTACCTTATATATAGATGCAATTCGAAACCC 720
    |||
DB 666 CAACCTTGACTCAATGAAAGCTTCCCTCCCTACCTTATATATAGATGCAATTCGAAACCC 725
OY 721 ACCCGTGAATGAGACCAATCTCTGATTTGGGCTGCTGCTGTAATGTTGGTCAATTTTG 780
    |||
DB 726 ACCCGTGAATGAGACCAATCTCTGATTTGGGCTGCTGCTGTAATGTTGGTCAATTTTG 785
OY 781 TGTGGGATGCTGTTCTTTCTTAACACTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
    |||
DB 786 TGTGGGATGCTGTTCTTTCTTAACACTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 845
OY 841 CATGAATGTGAAGCAACAAAGTGGAGAGAAAGGAGACCAACCAAGAGAGAGAGAGAGAG 900
    |||
DB 846 CATGAATGTGAAGCAACAAAGTGGAGAGAAAGGAGACCAACCAAGAGAGAGAGAGAGAG 905
OY 901 CGGTACCAATGAAAGCGGAAAGATCTGATGAAGCCAGTGTGTAACTTTTCAAGACAGCT 960
    |||
DB 906 CGGTACCAATGAAAGCGGAAAGATCTGATGAAGCCAGTGTGTAACTTTTCAAGACAGCT 965
OY 961 TCAGGCGACACAGTACTACACAGTTT 987
    |||
DB 966 TCAGGCGACACAGTACTACACAGTTT 992
    |||

RESULT 4
AAZ27914/c
ID AAZ27914 standard; DNA; 1897 BP.
XX
XX
AC AAZ27914;
XX
XX
DT 20-DEC-1999 (first entry)
XX
XX
DE Canine B7-2 gene complementary DNA sequence.
XX
XX
KM B7; CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;
KM allergic reaction; infectious disease; tumor development; canine;
KM graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
XX
OS Canis familiaris.
XX
XX
PN WO947558-A2.
XX
XX
PD 23-SEP-1999.
XX
XX
PF 19-MAR-1999, 99WO-US06187.
XX
XX
PR 19-MAR-1998; 98US-0078765.
XX
XX
PR 17-APR-1998; 98US-0062597.
XX
XX
PA (HESK-) HESKA CORP.
XX
XX
PI Sim G, Yang S, Sellins KS;
XX
XX
DR WPI; 1999-571822/48.
XX
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
```

```
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 101-102; 148pp; English.
XX
XX The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ Sequence 1897 BP; 529 A; 383 C; 400 G; 585 T; 0 other;

Query Match 100.0%; Score 987; DB 20; Length 1897;
Best Local Similarly 100.0%; Pred. No. 6,4e-287;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTATCTCAGATGCTACTATGAACTGAATTAACATTCCTTTGTGATGACCTCTGCTC 60
    |||
DB 1892 ATGTATCTCAGATGCTACTATGAACTGAATTAACATTCCTTTGTGATGACCTCTGCTC 1833
OY 61 TATGCTGCTGCTTCCATGAAGATCAAGCATATTTCAACAAGACTGAGAACTGCAATGC 120
    |||
DB 1832 TATGCTGCTGCTTCCATGAAGATCAAGCATATTTCAACAAGACTGAGAACTGCAATGC 1773
OY 121 CATTTTCAAATTCGCAAAACATTAAGCTGGATGAGTGGAGTGTGGAGAGAGAGAGAGAG 180
    |||
DB 1772 CATTTTCAAATTCGCAAAACATTAAGCTGGATGAGTGGAGTGTGGAGAGAGAGAGAGAG 1713
OY 181 GATAGCTGCTGTTCTGTACGACCTATACAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAG 240
    |||
DB 1712 GATAGCTGCTGTTCTGTACGACCTATACAGAGGCAAGAGAGAGAGAGAGAGAGAGAGAG 1653
OY 241 AAGTATGAAGGGCCGACAGACTTTGACAAAGACATTTGAGACCTGAGACTCCATTAATTT 300
    |||
DB 1652 AAGTATGAAGGGCCGACAGACTTTGACAAAGACATTTGAGACCTGAGACTCCATTAATTT 1593
OY 301 CAGATCAAGAGAGAGGGGTTGTATCATATGTTCTGTATCATTAAGGGCCCAAGGACTC 360
    |||
DB 1592 CAGATCAAGAGAGAGGGGTTGTATCATATGTTCTGTATCATTAAGGGCCCAAGGACTC 1533
OY 361 GTTCCCATGACACAGATGAATTTGACACTATACAGTGTGCTTAACCTCAACCTGAA 420
    |||
DB 1532 GTTCCCATGACACAGATGAATTTGACACTATACAGTGTGCTTAACCTCAACCTGAA 1473
OY 421 ATATGTAAGTCTTCTATATAGACGAAATTTCTGGCATCATTAATTTGACCTGCTCATCC 480
    |||
DB 1472 ATATGTAAGTCTTCTATATAGACGAAATTTCTGGCATCATTAATTTGACCTGCTCATCC 1413
OY 481 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGGTAAAAAACCGAGAATTCAGAT 540
    |||
DB 1412 ATACAAAGTTACCCAGAAACCCAGAGAGATGTAATTTTGGTAAAAAACCGAGAATTCAGAT 1553
OY 541 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATATATGTCACAGAACTCTACAACTT 600
    |||
DB 1352 ACTAAGTATGATACGTCTATGAAAGAAATCTCAAAATATATGTCACAGAACTCTACAACTT 1293
OY 601 TCTATCAGCTTGTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCTCTG 660
    |||
DB 1292 TCTATCAGCTTGTCTCTCTCACTCCCTGAGACCAATGTGAGCATCTCTCTGTCTCTG 1233
OY 661 CAACCTTGACTCAATGAAAGCTTCCCTCCCTACCTTATATATAGATGCAATTCGAAACCC 720
    |||
DB 1232 CAACCTTGACTCAATGAAAGCTTCCCTCCCTACCTTATATATAGATGCAATTCGAAACCC 1173
OY 721 ACCCGTGAATGAGACCAATCTCTGATTTGGGCTGCTGCTGTAATGTTGGTCAATTTTG 780
    |||
DB 1172 ACCCGTGAATGAGACCAATCTCTGATTTGGGCTGCTGCTGTAATGTTGGTCAATTTTG 1113
OY 781 TGTGGGATGCTGTTCTTTCTTAACACTAAGGAAAGGAGAGAGAGAGAGAGAGAGAGAGAG 840
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QY 61 TATGTCGCTGCTTCATGAGAGTCATATTTTCACAGACTGGAGACTGCCATGC 120
DB 927 TATGGTGGCTGCTTCATGAGAGTCATATTTTCACAGACTGGAGACTGCCATGC 868
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DB 867 CATTTTACAATTTCTCAAAACATTAAGCCCGATGAGTTGTTGTTTGGAGAGACCG 808
QY 181 GATTAAGCTGGTTCTGTACGAGCTATACAGAGGCAAGAGAACCCCAAAATGTTATGCG 240
DB 807 GATTAAGCTGGTTCTGTACGAGCTATACAGAGGCAAGAGAACCCCAAAATGTTATGCG 748
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DB 747 AAGTATTAAGGGGCGGCAACAGCTTTTACAAAGCAATTTGACCCCTGAGCTCATATAT 688
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DB 687 CAGATCAAGGAGCAAGGGCTGTATCAATGTTCTGTCATCAATTAAGGGGCGGCAAGGAGCTC 628
QY 361 GTTCCCATGCAACAGATGATGATTCGACCTATACAGTGTGCTTGAATCTCATCAACCTGAA 420
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QY 421 ATTAATGCTACTTCTTAATBGAACAGAAAATTTGCGCATCATTAATTTGACCTGCTCATCC 480
DB 567 ATTAATGCTACTTCTTAATBGAACAGAAAATTTGCGCATCATTAATTTGACCTGCTCATCC 508
QY 481 ATACAAGTTACCCAGAACCCCAAGAGATGATTTTGGTAAACCCGAGAAATTTCAAGT 540
DB 507 ATACAAGTTACCCAGAACCCCAAGAGATGATTTTGGTAAACCCGAGAAATTTCAAGT 448
QY 541 ACTAAGTATGATACTGTCATGAGAAATCTCAAAATTAATGTACAGAACTCTACAACTGT 600
DB 447 ACTAAGTATGATACTGTCATGAGAAATCTCAAAATTAATGTACAGAACTCTACAACTGT 388
QY 601 TCTATCAGCTTGTCTTCTCTCACTGCCCTAAGCAGCAATGTGAGCATCTTGTGCTCG 660
DB 387 TCTATCAGCTTGTCTTCTCTCACTGCCCTAAGCAGCAATGTGAGCATCTTGTGCTCG 328
QY 661 CAACCTTGATCAATGAGCACTTCCCTCCTACCTTATATATAGANTGCATACGAAACCC 720
DB 327 CAACCTTGATCAATGAGCACTTCCCTCCTACCTTATATATAGANTGCATACGAAACCC 268
QY 721 ACCCTGATGAGAGACACATCCTCTGATTCGCGCTGCTTGTAAATGTTGTCATTTTG 780
DB 267 ACCCTGATGAGAGACACATCCTCTGATTCGCGCTGCTTGTAAATGTTGTCATTTTG 208
QY 781 TGTGGGATGGTGTCTTCTTAACACTAAGGAAAGAAAGAAAGAGACAGCCCTGCCCTCT 840
DB 207 TGTGGGATGGTGTCTTCTTAACACTAAGGAAAGAAAGAAAGAGACAGCCCTGCCCTCT 148
QY 841 CATGAATGTGAACCAACAAAGTGGAGAAAGAAAGAAAGTGGAGACCAAGAAAGAGTA 900
DB 147 CATGAATGTGAACCAACAAAGTGGAGAAAGAAAGAAAGTGGAGACCAAGAAAGAGTA 88
QY 901 CGGTACCATGAAAGGAAAGATCTGATGAGCCCAAGTGTGTTAAATTTGGAAGACAGCT 960
DB 87 CGGTACCATGAAAGGAAAGATCTGATGAGCCCAAGTGTGTTAAATTTGGAAGACAGCT 28
QY 961 TCAGGCGCAACAGTACTACAGAGTTT 987
DB 27 TCAGGCGCAACAGTACTACAGAGTTT 1

```

RESULT 3
AA227913
ID AA227913 standard; DNA; 1897 BP.
XX

AC AA227913:
XX
DT 20-DEC-1999 (first entry)
XX

```

DE Canine B7-2 protein encoding DNA.
XX
KW B7; CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;
KW allergic reaction; infectious disease; tumor development; canine;
KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX
OS Canis familiaris.
XX
PN W09947558-A2.
XX
PD 23-SEP-1999.
XX
PF 19-MAR-1999; 99MO-US06187.
XX
PR 19-MAR-1998; 98US-0078765.
XX
PR 17-APR-1998; 98US-0062597.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Sellins KS;
XX
DR WPI: 1999-571822/48.
DR P-PSDB; AAY41076.
XX
PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases
XX
PS Claim 1; Page 97-99; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritis and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SO Sequence 1897 BP; 585 A; 400 C; 383 G; 529 T; 0 other;

Query Match 100.0%; Score 987; DB 20; Length 1897;
Best Local Similarity 100.0%; Pred. No. 6.4e-287;
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PT New isolated B7 and CTLA4 nucleic acids, used to develop products for
PT treating, e.g. autoimmune and atopic diseases -
XX
PS Claim 1; Page 102-103; 148pp; English.
XX
CC The invention provides B7 and CTLA4 (T cell costimulatory proteins)
CC encoding nucleic acid molecules from dogs and cats. The proteins can be
CC expressed by standard recombinant methodology. The nucleic acid molecules
CC and the encoded proteins can be used for preventing or treating diseases,
CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor
CC development, graft rejection, inflammation, arthritic and atopic diseases
CC such as atopic dermatitis. They can be used in mammals such humans, dogs,
CC cats, cattle, sheep or pets. The products can also be used for detection,
CC diagnosis and drug screening.
XX
SQ

Sequence 987 BP; 315 A; 215 C; 204 G; 253 T; 0 other;

Query Match 100.0%; Score 987; DB 20; Length 987;

Best Local Similarity 100.0%; Pred. No. 4.6e-287;

Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTATCTCAGATGCACTATGGAACATGATACATTCCTCTTTGTGATGACCCCTCGCTC 60
QY 61 TATGCTGCTGCTTCATGGAAGTCAGATATTTTCACAGACTGAGAACTGCCATGC 120
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DB 121 CATTTTACAAATTCACAAACATTAACCTCGATGACTGTGTGTTGGCAGACAG 180
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DB 241 AAGTATTAAGGGCGGCACAAAGCTTTGACAAACACAAATTTGACCCCTGACCTCAATAT 300
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QY 361 GTTCCCATGCAACAGATGATTCGACCTATGACCTGTTGCTAACTCACTCAACTGAA 420
DB 361 GTTCCCATGCAACAGATGATTCGACCTATGACCTGTTGCTAACTCACTCAACTGAA 420
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DB 421 ATTAATGTAAGTCTTAATAGAAAGAAATTCGSCATCAATAAATTTGACCTGCTATCC 480
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QY 781 TGTGGATGTTGTTCTTCTTAACACTAAGAAAGAGAAAGACGCTGCCCCCTCT 840
DB 781 TGTGGATGTTGTTCTTCTTCTTAACACTAAGAAAGAGAAAGACGCTGCCCCCTCT 840
QY 841 CATGAATGTGAACCAACAAAGTGAAGAAAAGAAAGTACAGACCAAGAAAGACTA 900
DB 841 CATGAATGTGAACCAACAAAGTGAAGAAAAGAAAGTACAGACCAAGAAAGACTA 900
QY 901 CGGTACCATGAACCGAAGATGATGAAGCCCACTGTGTTAACTTTCGAAGACAGCT 960
DB 901 CGGTACCATGAACCGAAGATGATGAAGCCCACTGTGTTAACTTTCGAAGACAGCT 960
QY 961 TCAGGCGACACAGTACTACACAGTTT 987
DB 961 TCAGGCGACACAGTACTACACAGTTT 987
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RESULT 2

AA227916/c

ID AA227916 standard; DNA; 987 BP.

XX AA227916;

AC 20-DEC-1999 (first entry)

DT Complementary strand of canine B7-2 coding sequence.

XX B7: CTLA4; T cell costimulatory protein; dog; cat; autoimmune disease;

XX allergic reaction; infectious disease; tumor development; canine;

KW graft rejection; inflammation; arthritis; atopic dermatitis; ss.

OS Canis familiaris.

XX WO947558-A2.

PN 23-SEP-1999.

XX 19-MAR-1999; 99WO-US06187.

PF 19-MAR-1998; 98US-0078765.

PR 17-APR-1998; 98US-0062597.

XX (HESK-) HESKA CORP.

PA Sim G, Yang S, Sellins KS;

PI WPI; 1999-571822/48.

XX New isolated B7 and CTLA4 nucleic acids, used to develop products for

PT treating, e.g. autoimmune and atopic diseases -

XX Claim 1; Page 103-104; 148pp; English.

PS The invention provides B7 and CTLA4 (T cell costimulatory proteins)

CC encoding nucleic acid molecules from dogs and cats. The proteins can be

CC expressed by standard recombinant methodology. The nucleic acid molecules

CC and the encoded proteins can be used for preventing or treating diseases,

CC e.g. autoimmune diseases, allergic reactions, infectious diseases, tumor

CC development, graft rejection, inflammation, arthritic and atopic diseases

CC such as atopic dermatitis. They can be used in mammals such humans, dogs,

CC cats, cattle, sheep or pets. The products can also be used for detection,

CC diagnosis and drug screening.

XX Sequence 987 BP; 253 A; 204 C; 215 G; 315 T; 0 other;

SQ

Query Match 100.0%; Score 987; DB 20; Length 987;

Best Local Similarity 100.0%; Pred. No. 4.6e-287;

Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTATCTCAGATGCACTATGGAACATGATACATTCCTCTTTGTGATGACCCCTCGCTC 60
QY 987 ATGTATCTCAGATGCACTATGGAACATGATACATTCCTCTTTGTGATGACCCCTCGCTC 928
DB 987 ATGTATCTCAGATGCACTATGGAACATGATACATTCCTCTTTGTGATGACCCCTCGCTC 928
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 17:31:44 ; Search time 149.213 Seconds
(without alignments)
11356.866 Million cell updates/sec

Title: US-09-646-561-9

Perfect score: 987
Sequence: 1 atgatacagatcagacta.....acaacagctactacagttt 987

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	987	100.0	987	AA227915	Canine B7-2 protei
2	987	100.0	987	AA227916	Complementary str
3	987	100.0	1897	20 AA227913	Canine B7-2 protei
4	987	100.0	1897	20 AA227914	Canine B7-2 gene c
5	784.8	79.5	996	20 AA227931	Feline B7-2 protei
6	784.8	79.5	996	20 AA227932	Complementary str
7	784.8	79.5	2830	20 AA227929	Feline B7-2 protei
8	784.8	79.5	2830	20 AA227930	Feline B7-2 gene c
9	772.8	78.3	21	AA234838	Feline CD86 (B7-2)

10	772.8	78.3	1080	21	AA234785	Cat CD86 (B7-2) cD
11	704	71.3	840	20	AA227923	Canine B7-2S prote
12	704	71.3	840	20	AA227924	Complementary str
13	704	71.3	1795	20	AA227921	Canine B7-2S prote
14	704	71.3	1795	20	AA227922	Canine B7-2S gene
15	621	62.9	1050	21	AA49661	Pig costimulatory
16	575.2	58.3	1120	16	AA081351	Human B lymphocyte
17	575.2	58.3	1120	16	AA49181	Human B lymphocyte
18	575.2	58.3	1120	20	AAV55784	Human B7-2 antigen
19	575.2	58.3	1120	21	AA084049	Human B lymphocyte
20	570.2	57.8	1424	21	AA229321	Human B7-2 cDNA
21	570.2	57.8	1428	16	AA085873	B70 type B antigen
22	570.2	57.3	2205	22	AAH72616	Human cervical can
23	565.2	57.3	972	20	AAV83208	B7-2 cDNA. Homo s
24	565.2	57.3	972	24	AA025510	Human co-stimulat
25	484.6	49.1	764	18	AA062939	Chimeric human/po
26	463.8	47.0	831	19	AAV03230	DNA encoding CD86
27	453.8	46.0	738	20	AAV80293	Human B7-2 extrac
28	453.8	46.0	738	22	AAE89731	Nucleotide sequenc
29	369.8	37.5	509	20	AA227933	Feline B7-2 protei
30	369.8	37.5	509	20	AA227934	Feline B7-2 gene (
31	344.4	34.9	1151	20	AAV55785	Mouse B7-2 antigen
32	344.4	34.9	1163	18	AA49182	Mouse B lymphocyte
33	344.4	34.9	1163	21	AA084050	Murine B lymphocyt
34	342.8	34.7	1163	16	AA081366	Murine B lymphocyt
35	337.2	34.2	1261	16	AA01046	Mouse B7-2 constan
36	329.2	33.4	942	19	AAE9926	Rat CD86 coding se
37	265.8	26.5	403	20	AAV89569	EST clone CR506.
38	232.4	23.5	330	18	AA49197	Human B lymphocyte
39	232.4	23.5	330	21	AA084082	Human B7-2 variabl
40	218	22.1	450	21	AA00427	Human secreted pro
41	175.2	17.8	306	18	AA49198	Human B lymphocyte
42	175.2	17.8	306	21	AA084083	Human B7-2 constan
43	169.4	17.2	339	20	AA227935	Feline B7-2 protei
44	169.4	17.2	339	20	AA227936	Feline B7-2 gene (
45	103.4	10.5	210	16	AA01038	Human B7-2 exon 5.

ALIGNMENTS

RESULT 1	
AA227915	
ID	AA227915 standard; DNA: 987 BP.
XX	
AC	AA227915:
XX	
DT	20-DEC-1999 (first entry)
XX	
DE	Canine B7-2 protein coding sequence.
XX	
XX	
KW	B7: CTLA4: T cell costimulatory protein; dog; cat; autoimmune disease;
KW	allergic reaction; infectious disease; tumor development; canine;
KW	graft rejection; inflammation; arthritis; atopic dermatitis; ss.
XX	
OS	Canis familiaris.
XX	
PN	WO9947558-A2.
XX	
PD	23-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06187.
XX	
PR	19-MAR-1998; 98US-0078765.
XX	
PR	17-APR-1998; 98US-0062597.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Slim G, Yang S, Sellins KS;
XX	
DR	WPI, 1999-571822/48.
XX	
DR	P-PDB; AAY41076.
XX	

Matches	156;	Conservative	0;	Mismatches	42;	Indels	6;	Gaps	2;
OY	790	GTGTTCTTTCTTACACTAAGAAA--AGGAAGAAAGACACCCCTGCCCTCTCATGAA							846
Db	504	GTTTTCCTGTCTAATTCCTATGTAGAAATGGAAGAAGAAAGAGCGGCTCGCAACTTATATAA							445
OY	847	TGTGAACCAACAAGTGTGAGAGAAAGAAAGTGTGACAGACCAGAGAAAGATACGGTAC							906
Db	444	TGTGACACCAACACATGTGAGAGGAGAGAGATGTACAGACCAGAGAAAGAGAAAAAATC							385
OY	907	CATGAAGCGAAAGATCTGTATGATGATGCCCAAGTGTG--TTACATTTGNAAGACAGCTTCA							963
Db	384	CATATACCTGAAAGATCTGTATGATGAAACCAACGCGTGTTTTAAAGTTCGAGACATCTTCA							325
OY	964	GGCGACACACGACTACTACACAGTTT	987						
Db	324	TCCGACAAAAGTGATGATGTTT	301						
RESULT 15									
LOCUS	BF171298		314 bp	mRNA	linear	EST 23-MAR-2001			
DEFINITION	PCI2416 Myeloma (PCL) cDNA library Homo sapiens cDNA, mRNA								
ACCESSION	BF171298								
VERSION	BF171298.1	GI:13437512							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE	1 (bases 1 to 314)								
AUTHORS	Claudio,J.O., Tang,H., Khan,E.M., Voralia,M., Li,Z., Cukerman,E.,								
	Francisco-Pabalan,O., Biew,C.C. and Stewart,A.K.								
TITLE	The transcriptional phenotype of myeloma cells								
JOURNAL	Unpublished (2000)								
COMMENT	Contact: A. Keith Stewart, M.D.								
	Oncology Research								
	University Health Network								
	610 University Ave., 5-126, Toronto, Ontario, Canada								
	Tel: (416) 946-4639								
	Fax: (416) 946-6546								
	Email: k.stewart@utoronto.ca								
	PCR Primers								
	FORWARD: 5'-GCCAAGCTCGAAATTAACCTCAGTAAGG-3'								
	BACKWARD: 5'-CCAGTGATGTATACGACTCACTATAGGCG-3'								
	Seq primer: 5'-GAATTAACCTCACTAAGG-3'								
FEATURES	Location/Qualifiers								
SOURCE	1..314								

`/dev.stage="lambda cell leukemia"`
`/note="vector: lambda Zap Express; Site_1: EcoRI; Site_2:`
`theta; mRNA was purified from plasma cell leukemia`
`patient's peripheral blood containing >95% myeloma. An`
`oligo d(TT)18 primer containing XhoI restriction site was`
`used to prime first strand synthesis using M-MLV reverse`
`transcriptase. To protect the cDNAs from XhoI digestion in`
`subsequent cloning step, the nucleotide analogue`
`5-methyl-dCTP was added to the nucleotide mixture and`
`a 32P-dATP was added to monitor the quantity and quality`
`of first strand synthesis. After second strand synthesis`
`and blunting of cDNA termini, EcoRI adapters were ligated`
`and followed by kinase treatment and digestion with XhoI.`
`The cDNAs were then size-fractionated using Sephacryl`
`S-500 column and then ligated into EcoRI and XhoI digested`
`lambda Zap Express vector. The ligation product was`
`packaged using Gigapack II packaging extract. The library`
`had primary titre of approx. x106. Clones from the`

```

primary library were randomly selected for single pass
sequencing."
BASE COUNT      68 a      70 c      74 g      102 t
ORIGIN
Query Match      10.6%; Score 104.2; DB 10; Length 314;
Best Local Similarity 77.3%; Pred. No. 6.7e-17;
Matches 140; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY      14 GCACATGGAACGTGAATTAACATTCCTCTTTGGATGACCCCTCGTCTATGATGCTGCTT 73
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      125 GCACATATGGGACTGAGTACACTTCCTCTTTGATGAGCCCTTCTGCTCTGTGCTGCTT 184

QY      74 CCATGAGAGTCCAACCATATTTCAACAAGACTGGAGAACTGCCATGCCATTTTACAAATT 133
        || ||| |||| ||| || ||| ||||| ||||| ||||| ||||| |||||
Db      185 CTCGTAGAGTTTAAGCTTATTATGAGACTC--AGACCTGCGATGCCAATTTGCAAACT 241

QY      134 CTCAAACAATAAGCTGGATGAGTTGGTAGTGTTTGGCAGAGACCAGATAAGCTGGGTTTC 193
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      242 CTCAAACCAAAAGCCTGAGTGAAGTAGATATTTTGGCAGAGACCAGAAACCTTGGTTTC 301

QY      194 T 194
Db      302 T 302

Search completed: October 20, 2002, 04:29:38
job time : 1192.32 secs

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Search completed: October 20, 2002, 04:29:38
Job time : 1192.32 secs

OY	924	TGATGAACCCCAAGCTGTG---TTAAATTTCGAGAAGACTTTCAGCGCACAACAGTACTAC	980
Db	313	TGATGAACCCCAAGCTGTGTTTTTAAAAAGTTCGAAGACATCTTCATGCACAAAAGTGATAC	372
OY	981	ACAGTTT	987
Db	373	ATGTTT	379
RESULT	11		
LOCUS	BG001664	347 bp	mRNA linear EST 24-JAN-2001
DEFINITION	RCL-GN0067-151100-016-b07 GN0067 Homo sapiens CDNA, mRNA sequence.		
ACCESSION	BG001664		
VERSION	BG001664.1	GI:12440219	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 347)		
	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,,		
	Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,		
	Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,		
	Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare		
	,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and		
	Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed		
JOURNAL	sequence tags		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
COMMENT	20202663		
	Contact: Simpson A.J.G.		
	Laboratory of Cancer Genetics		
	Ludwig Institute for Cancer Research		
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,		
	Brazil		
	Tel: +55-11-2704922		
	Fax: +55-11-2707001		
	Email: asimpson@ludwig.org.br		
FEATURES	This sequence was derived from the FAPESP/LICR Human Cancer Genome		
Source	Project. This entry can be seen in the following URL		
	(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC4&l2=RC4-GN0067		
	151100-016-b07&t3=2000-11-15&l4=1)		
	Seq primer: puc 18 forward		
	High quality sequence start: 19		
	High quality sequence stop: 347.		
	Location/Qualifiers		
	1..347		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_lib="GN0067"		
	/dex_stage="Adult"		
	/note="Organ: Placenta.normal; Vector: puc18; Site_1: SmaI		
	; Site_2: SmaI; A mini-library was made by cloning		
	products derived from ORESTES PCR (U.S. Letters Patent		
	application No. 196,716 - Ludwig Institute for Cancer		
	Research) profiles into the puc 18 vector. Reverse		
	transcription of tissue mRNA and cDNA amplification were		
	performed under low stringency conditions."		
BASE COUNT	109 a	75 c	75 g
ORIGIN	88 t		
Query Match	12.7%	Score 125.6;	DB 10; Length 347;
Best Local Similarity	62.6%;	Pred. No. 1.5e-22;	
Matches 231; Conservative	0;	Mismatches 89;	Indels 12; Gaps 4
OY	638	ATGTGACATCTTCTGTCTCTCGTCAACTTGAGCTCATGAGCTCCCTCCCTACCTTANA	697
Db	21	ATATGACCATCTTCTGTATTTGTAACAGTGAACGACGGCGTTTATCTTCACCTTCT	80
OY	698	ATATGATGACATATCGAAACCACCCCTCAGTAGAGACCATCTCTTGATTTGGCGCTC	757

Db	Accession	Source	Score	Length	Gap
Db	81 CTACAGA---GCTTGAAGACCCCTCAGCCCTCCGCCAGACACATTCCTTGATATACAGCTG	137			
Qy	758 TGCCTGTAATGTTGCTCATTTTGTGTGGGANGTGTTCTTTCTTAACACTTAAGAAA---A	814			
Db	138 TACTTCCCAACA---GTTATTATATGTGTGATGGTTTCTGTCTTAATTGTATGGAATGA	194			
Qy	815 GGAAGAACAGAGAGCGCTGGCCCTCATGTGATGTGAAGCAACAAGGAGAGAAAG	874			
Db	195 AGAGAACAGAGAGCGCTGGCAACTTTTAAATGTGTGGAACCAACCAATGTGAGAGGAA	254			
Qy	875 AAAGTACAGACCAAGAAAGTAGTCGTACCATGAAACGGAAGATCTGATGAAGCC	934			
Db	255 AGAGTAGACAGACCAAGAAAGAAATTCATATACGTGAAGATCTGATGAAGCC	314			
Qy	935 AGTGTG---TTAACATTCGAAAGACAGCTCA	963			
Db	315 AGCGTGTTTTAAAGTTCCGAAGACATCTTCA	346			
RESULT 12					
LOCUS	BF064222/c				
DEFINITION	BF064222	543 bp	linear	EST 16-OCT-2000	
ACCESSION	7f57b02.31	Soares_NSF_F8_9W_OT_PA_P_S1	Human sapiens	CDNA clone	
VERSION	IMAGE:3390507	3	Similar to SW:CD86, HUMAN P42081	T LYMPHOCYTE	
KEYWORDS	ACTIVATION	ANTIGEN CD86	PRECURSOR	;	mRNA sequence.
SOURCE	BF064222				
ORGANISM	BF064222.1	GI:10823132			
REFERENCE	human.				
AUTHORS	Homo sapiens				
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
COMMENT	1 (bases 1 to 543)				
FEATURES	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
	Tumor Gene Index				
	Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: c9apbs@remail.nih.gov				
	This clone is available royalty-free through LNL ; contact the				
	IMAGE Consortium (infoimage.lnl.gov) for further information.				
	Seq primer: -40UP from Gibco				
	High quality sequence stop: 496.				
	Location/Qualifiers				
	1..543				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:3390507"				
	/clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"				
	/lab_host="DH10B"				
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with				
	a modified polylinker; Site:1: Not I; Site:2: Eco RI;				
	Equal amounts of plasmid DNA from five normalized				
	libraries were mixed, and ss circles were made in vitro.				
	Following HAP purification, this DNA was used as tracer in				
	a subtractive hybridization reaction. The driver was				
	PCR-amplified cDNAs from pools of 5,000 clones made from				
	the same 5 libraries. The pools consisted of the following				
	libraries and clones: Soares NBHSF pool 1:				
	309384-310919, 323208-325895 Soares NB2HP pool 1:				
	145032-147335, 147720-148103, 148872-149255, 15002 -				
	150407, 151176-152327 Soares NB2HF8-9W pool 1:				
	75880-760583, 772104-774407 Soares NBHPA pool 1:				
	304776-306311, 320136-322823 326380-326653 Soares NBHPT				
	pool 1: 723720-726407, 739080-740999 Subtraction by Benc				
	Soares and M. Fatima Bonaldo."				
ORIGIN	151 a	104 c	112 g	175 t	1 others
Query Match	11.8%	Score 116.4	DB 10;	Length 543;	
Best Local Similarity	76.6%	Pred. No. 4.7e-20;			
Matches 170;	Conservative	0;	Mismatches 46;	Indels 6;	Gaps 2;

Db	636	CAGACATTACGACTGT	654
RESULT_9			
LOCUS	AM427922	257 bp	mRNA linear EST 25-APR-2001
DEFINITION	64549 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.		
ACCESSION	AM427922		
VERSION	AM427922.1	GI:695869	
KEYWORDS	EST.		
SOURCE			
ORGANISM	Bos taurus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
Bovidae; Bovinae; Bos.			
1 (bases 1 to 257)			
Smith,T.P.L., Grosse,W.M., Feking,B.A., Roberts,A.J., Stone,R.T.,			
Casas,E., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C., Bennett,			
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,			
Pertea,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and			
Keele,J.W.			
Sequence evaluation of four pooled-tissue normalized bovine cDNA			
libraries and construction of a gene index for cattle			
Genome Res. 11 (4), 626-630 (2001)			
21180013			
Contact: Smith TPL			
USDA, ARS, US Meat Animal Research Center			
PO Box 166, Clay Center, NE 68933-0166, USA			
Tel: 402 762 4356			
Fax: 402 762 4350			
Email: smith@email.marc.usda.gov			
Single pass sequencing. Bases called and trimmed with phred			
v0.980904.e. Vector identified by cross_match with the -minscore 20			
and -maxlength 12 options.			
PCR primers			
FORWARD: AGCAACAGCTATGCAT			
BACKWARD: GTTTCCAGTCACGACG			
Plate: 30 row: G column: 20			
Seq primer: ATTAGGTGACACTAATG.			
Location/Qualifiers			
1..257			
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/db_xref="taxon:9913"			
/clone_lib="MARC 3BOV"			
/tissue_type="pooled"			
/lab_host="DH10B"			
/note=Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;			
Library made from pooled tissue from marrow, alveolar			
macrophage, ovary, fetal semitendinosus muscle, and fetal			
Longissimus muscle."			
BASE COUNT	80 a	64 c	61 t
ORIGIN			
Query Match	17.8%;	Score 176;	DB 9; Length 257;
Best Local Similarity	80.5%;	Pred. No. 6.3e-36;	
Matches 206; Conservative	0; Mismatches 50; Indels 0; Gaps 0;		
QY	112	CTGGCATGCCATTTTACAATAATTCATAAAACATTAAGCCGTGATGTTGGT	171
	2	CTGGCATGCCATTTTCCAACACCACCAAACTCAGCCTCGACGAACGTGATATTTTGG	61
QY	172	CAGGACCAAGATTAAGCTGGTCTGTACGAGCTATACAGAGCAAAGAAGAACCCCAAAAT	231
	62	CAGGATCAAGATTAAGTGTTCTCTTAGAGCTATTCAAAAGGCCAAAGAGGACCAATTAAT	121
QY	232	GTTCATGCCAAGTTAAGGGCGCACAGCTTTGATCAATGTTTCGTCATCAATTAAGGGCCC	291
	122	GTTCATGCCAAGTTAAGGGCGCACAGCTTTGATCAATGTTTCGTCATCAATTAAGGGCCC	351
QY	292	CATAATTTGAGATCAAGGACCAAGGCTTGATCAATGTTTCGTCATCAATTAAGGGCCC	351
	182	CACAAGCTTAACATCAAGACACAGGCTCGATTAATGTTTCAATCCATCATAGAGGCTCC	241

[illegible]

OY	610	TTGTCTTTCAGTGAGTCCCGGACGAACAATGAGACATCTTGTGTCTGCACCTTAG	669
Db	393	GTGTCTTCCCATCCCTCCGACCAATATGAGCATTNGCTGTCTCCAATTGAG	334
OY	670	TCAATGAA-----GCTTCCCCTACCCTATATATAGATGCA---CATACGAAACC	720
Db	333	CCAACGAGACACTGTTTTCTTCCTTACCTTGTATATATAGATGCAAGCCACTGTGCA	274
OY	721	ACCCCTGATGAGACACATCCCTGATTTGGCTGCTGTTAATGTGGTCATTTTG	780
Db	273	CCCCCTGCCAGACACATCCTTNGATGTGAGCTTACTTTGTAACAGTGGTGTGTG	214
OY	781	TGTGGATGATGTTCTTTCTTAACACTAAGAAGAAAGAACAGCACCTTGGCCCTCT	840
Db	213	TGTGGATGATGTTCTTTCTTAACACTAAGAAGAAAGAACAGCACCTTGGCCCTCT	154
OY	841	CATGAT---GTGAACCAACCAACTGGAGAAAAGAAAGAGAGACACCAAGGAAGA	897
Db	153	AATGATGTGTGATGGAACCATCAAATGAAACAGAGAGGCGAGTGAACAATTAAGACGA	94
OY	898	GTAAGGTAACATGAAGGAAAGATCTGATGAAGCCAGTG---TGTTAAGATTTGCAAG	954
Db	93	AGTCAAT-----GAAGATCTGATGATGCGCCAGTGATGATTAATATTTNAG	45
OY	955	ACAGCTCAGGCGACACAGTACTACAGATTT	987
Db	44	ACAGCTCAGATGACACAGTACTACAGATTT	12
RESULT 8			
LOCUS	Bb635605	654 bp	mRNA linear EST 26-OCT-2001
DEFINITION	Bb635605 RIKEN full-length enriched, 0 day neonate thymus Mus musculus CDNA A430076L06 5', mRNA sequence.		
ACCESSION	Bb635605		
VERSION	Bb635605.1	GI:16471650	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Arakawa,T., Carinici,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,T., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
JOURNAL COMMENT	Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Shuho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ Carinici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of csp-trapper-selected cdnas to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) waghi,K., Fujiwake,S., Inoue,K., Togawa,Y., Itawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer. Genome Res. 10 (11), 1757-1771 (2000)		

		Kono H., Fukunishi Y., Shibata K., Itoh M., Carninci P., Sugahara Y., and Hayashizaki Y.
		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11(2), 281-289 (2001)
		Kondo S., Shinagawa A., Saito T., Kiyosawa H., Yamakura I., Alzawa K., Fukuda S., Hara A., Itoh M., Kawai J., Shibata K. and Hayashizaki Y.
		Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
FEATURES		Location/Qualifiers
SOURCE		1. 654 /organism="Mus musculus" /db_xref="taxon:10090" /clone="AA30076L06" /clone.lib="RIKEN full-length enriched, 0 day neonate thymus" /tissue_type="thymus" /dev_stage="0 day neonate" /lab_host="DH10B"
		/note="Site.1: SalI; Site.2: BamHI; CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand CDNA was primed with a primer [5' GAGAGA GAGAGATCCACAGAGCCTTTTTTTTGTNN 3'] CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand CDNA was prepared with the primer adapter of sequence [5' GAGAGA GAGATTGCAGTTTAATAATATCCCCCCCCCC 3']. CDNA was cleaved with XhoI and BamHI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PLC I."
BASE COUNT	148 a 151 c 152 g 202 t 1 others	
ORIGIN		
Query Match	20.6%; Score 203.6; DB 9; Length 654;	
Best Local Similarity	71.0%; Pred. No. 4.2e+43;	
Matches 269; Conservative	0; Mismatches 110; Indels 0; Gaps 0;	
OY	13 TGCACATGAGCAACAATGAATCATTCCTCTTGATGAGACCCTCCCTCGCTATGSGCTGCT 72 	
Db	276 TGCAACATGGCGCTTGCCAATCCTAATCTTTGAGAGACTTGCTGATATCGAGTCTGTT 335 	
OY	73 TCACATGAGAGTAGCAACATATTTCAACAAGACTGAGAGACTGCCATTCATTTCAACAT 132 	
Db	336 TCCGTTGAGAGCAAGCTTATTTCAATGGAGCTGCATATCTGCCCTGCCCATTGCAAAG 395 	
OY	133 TTCTCAAACATPAAGCCTGATGATGTTGTTAGTGTGTTGGCAGAGACCAGAGATATGGTT 192 	
Db	396 GCTCAAAACATPAAAGCCTAGTGAAGCTGTAGTATTTTGGCAGACCAAAAAGTTGGTT 455 	
OY	193 CTGTACGAGCTTTACAGAGCAAAAGAAAGACCTCAAAATGGTACATCGCAAGATPAAGGGC 252 	
Db	456 CTTGTACGAGCACTATTTTGGGCACADAAGAAACTGTATGTTGAATGCCAAGTACTGGC 515 	
OY	253 CGCACAGAGCTTTGACAAAGACATTTGACACCTGAGACTTCATATATTTCAGATCAGAGAC 312 	
Db	516 CGCACAGAGCTTTGACAGCAACAGCAAGCTGTACACATTCACAAATGTTCCAGATCAAGAGC 575 	
OY	313 AAGGCGTTGATCATGTGTTGTTCAATCATATPAAGGCGCCCAAGAGCTCGTTCCATGCAC 372 	
Db	576 ATGGGCTGTATGATGTTGTTTATACAAAAAAGCCACCACAGATCAATTTATCTTCCA 635 	
OY	373 CAGATGAATTCTGACCTAT 391 	

[illegible]

QY	456	CATCAATAATTTGACCTGCTCATTCATCA	486	
Db	420	--TCATAAATTTGACCTGCTCATTCACAA	448	
RESULT 4				
LOCUS	BB631711	629 bp	mRNA linear EST 26-OCT-2001	
DEFINITION	BB631711 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA A130091H03 5', mRNA sequence.			
ACCESSION	BB631711			
VERSION	BB631711.1	GI:16468418		
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus. 1 (bases 1 to 629)			
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.			
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagii,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.			
FEATURES	Location/Qualifiers			
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	/note="Site.1: SalI. Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia			

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:33:50 ; Search time 1176.32 Seconds

(without alignments)
11324.679 Million cell updates/sec

Title: US-09-646-561-9

Perfect score: 987

Sequence: 1 atgtatctcagatgcactat.....acaacagctactacagcttt 987

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
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16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	358	36.3	655	10	BI824940 603032554
3	323.8	32.8	448	9	AA056906 EST224R P
4	281.4	28.5	629	9	BB631711 BB631711
5	263.2	26.7	1002	10	BF137460 601780644
6	257.2	26.1	578	10	BM089797 503647 MA
7	243	24.6	512	9	AA056905 EST224F P
8	203.6	20.6	654	9	BB635605 BB635605
9	176	17.8	257	9	AA427922 64549 MAR
10	144.6	14.7	496	9	AA516826 xg04H01 X
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ALIGNMENTS

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DEFINITION mRNA sequence.
ACCESSION BI906246
VERSION BI906246.1 GI:16168907
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE Unpublished (1999)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM11533 row: 0 column: 17
High quality sequence stop: 719.
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non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

FEATURES

source

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VERSION	ARI46413.1	GI:15109602		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1120)			
AUTHORS	Sharpe,A.H., Borriello,F., Freeman,G.J. and Nadler,L.M.			
TITLE	B7-1 and B7-2 polypeptides			
JOURNAL	Patent: US 6218510-A 22 17-Apr-2001;			
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Db	484	ATACAGGTTACCCAGAACCCAGAGATGATGATTTTTTGGTAAAGCAAGAATTCACCT	543	ILETKTRLLSPFSLIELEDPPDPDHLPMWTAFLPVIIICVWFCLIKMKKKRP	
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DEFINITION	Human CTIL4 counter-receptor (B7-2) mRNA, complete cds.				
ACCESSION	L25259				
VERSION	L25259.1	GI:416368			
KEYWORDS	CTIL4 counter-receptor.				
SOURCE	Homo sapiens	cDNA to mRNA.			
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 1112) Freeman,G.J., Gribben,J.G., Boussioutis,V.A., Ng,J.W., Restivo,V.A., Jr., Lombard,L.A., Gray,G.S. and Nadler,L.M.				
TITLE	Cloning of B7-2: a CTL4 counter-receptor that costimulates human T cell proliferation [see comments]				
JOURNAL	Science 262 (5135), 909-911 (1993)				
MEDLINE	94053735				
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DEFINITION Sequence 33 from patent US 6251627.
ACCESSION ARI59758
VERSION ARI59758.1 GI:16222530
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1002)
AUTHORS Cai,Z., Sprent,J., Brummark,A., Jackson,M. and Peterson,P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6251627-A 33 26-JUN-2001;
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Location/Qualifiers
source 1..1002
BASE COUNT 309 a 215 c 203 g 275 t
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Query Match 58.3%; Score 575.2; DB 6; Length 1002;
Best Local Similarity 77.8%; Pred. No. 6.7e-144;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

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DB 67 TCTGTTGCTGCTCTCTCAATGATTCACATTTTCAATGAGCTGACAGCTCCCATGC 126
OY 121 CATTTTAAATTTCTCAAAACATTAAGCCTTGATGAGTGTGATGTTTGGCAGACCA 180
DB 127 CAATTGGAAACTCTCAAAACCAAGCCTGAGTGAGCTAGTAGTATTTTGGCAGACCA 186
OY 181 GATAAGCTGTTCTGTACAGCTATACAGAGCAAGAAAGCAACCTCAAAATGTTTCATGC 240
DB 187 GAAACTGTTGTTCTGATAGAGTATCTTAGCAAGAAAGAAATTTGACAGTTCATTC 246
OY 241 AAGTTAAGGGCCGACAGCTTTGACAAAGCAATTTGGACCTTGAGACTCCATAATTT 300
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DEFINITION Sequence 33 from patent US 6255073.
ACCESSION ARI60450
VERSION ARI60450.1 GI:16224366
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1002)
AUTHORS Cai,Z., Sprent,J., Brummark,A., Jackson,M. and Peterson,P.A.
TITLE Antigen presenting system and methods for activation of T-cells
JOURNAL Patent: US 6255073-A 33 03-JUL-2001;
FEATURES
Location/Qualifiers
source 1..1002
BASE COUNT 309 a 215 c 203 g 275 t
ORIGIN

Query Match 58.3%; Score 575.2; DB 6; Length 1002;
Best Local Similarity 77.8%; Pred. No. 6.7e-144;
Matches 775; Conservative 0; Mismatches 203; Indels 18; Gaps 6;

OY 1 ATGTATCAGATGCACTATGAACTGAATAACATTCCTTTGTGATGACCCCTGCTC 60
DB 7 ATGATGCCCAAGTGACTATGGAAGTAAACATTCCTTTGTGATGACCCCTGCTC 66
OY 61 TATGTCGCTGCTTCATGAAGAGTCAAGCATATTTCAACAGACTGAGAACTGCATGC 120
DB 67 TCTGTCGCTGCTCTCTGGAAGATTCAGCTTATTTCAATGAGAGCTCAACCTGCATGC 126
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Db 838 GGTGAACCAACAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 897
QY 907 CATGAACGGAAGATCTGATGAAGCCCATG---TCTTAACATTCGAGAGAGAGAGAGAG 963
Db 898 CAT-----GAGCATCTGATGATGCCAGTGTGATGTTAATTTAAAGACAGCCTCA 951
QY 964 GCGGACAACAGTACTACACAGTTT 987
Db 952 GATGACAACAGTACTACAGATTTT 975
RESULT 7
AX027016 994 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 13 from Patent WO00377102.
ACCESSION AX027016
VERSION AX027016.1 GI:10188045
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 994)
Rogers,N.J., Dorrling,A. and Lechler,R.I.
Immunosuppression
Patent: WO 0037102-A 13 JUN-2000;
ROGERS NICHOLA JANE (GB) ; DORRLING ANTHONY (GB) ;
LECHLER ROBERT IAN (GB)
FEATURES
Location/Qualifiers
1..994
/organism="Sus scrofa"
/db_xref="taxon:9823"
BASE COUNT 302 a 241 c 202 g 249 t
ORIGIN
Query Match 62.8%; Score 620; DB 6; Length 994;
Best Local Similarity 81.3%; Pred. No. 6e-156;
Matches 800; Conservative 0; Mismatches 160; Indels 24; Gaps 6;
QY 19 ATGAGCAATGAATTAACATCTCTTGTGTGATGACCCCTGCTCTATGTCCTCTCCATG 78
Db 1 ATGGAGCTGAGTACATCTCTTGTGTGATGCTCTCTGCTCTGCTCTCTCTCTCTCTG 60
QY 79 AAGAGTCAAGCATATTTCAACAAGAGTGGAGAACTGCCATTTTCAATTTCTCA 138
Db 61 AAAAGTCAGGCAATTTTCAATGATGAGAGAACTGCCCTGCTTTTCAACACTCGCAG 120
QY 139 AACATAGCCTGGAGTGTGTGTGTTGGCAGAGCAGATATAGCTGTCTGTAC 198
Db 121 AACCTAAGCTGATGAGCTGCTCATATTTGGCAGAGCAGAGATTAACCTGTCTCTAC 180
QY 199 GAGCTTACAGAGGCAAGAGAAAGCCCTCAATGTTCAATGCAAGATTAAGGGCCGACA 258
Db 181 GAGCTATACGAGGCGCAAGAGAAAGCCCTCAATATATGTTAATTCGAATATATGAGTGCACA 240
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	Matches	707: Conservative	0: Mismatches	5: Indels	0: Gaps	0:
QY	1	ATGTATCTCAGATGACATATGAGACTGATAATACATCTCTTGTGTGATGACCTCTGCTC	60			
Db	7	ATGTATCTCAGATGACATATGAGACTGATAATACATCTCTTGTGTGATGACCTCTGCTC	66			
QY	61	TATGTGCTGCTTCATGAGAGTCAGACATATTTTCAACAGACTGAGAACTGCCATGC	120			
Db	67	TATGTGCTGCTTCATGAGAGTCAGACATATTTTCAACAGACTGAGAACTGCCATGC	126			
QY	121	CATTTTACAAATTCACAAACATATAGCCGTGGATGGTGGTAGTGGTTTTGGAGGACAG	180			
Db	127	CATTTTACAAATTCACAAACATATAGCCGTGGATGGTGGTAGTGGTTTTGGAGGACAG	186			
QY	181	GATTAAGCTGTTCTGTAGAGAGCTATACAGAGCAAGAAGAACTCTCAAAATGTTATGCG	240			
Db	187	GATTAAGCTGTTCTGTAGAGAGCTATACAGAGCAAGAAGAACTCTCAAAATGTTATGCG	246			
QY	241	AAGTATTAAGGGCCGCACAAAGCTTTGACAAAGCAATTTGACCTTGAGACTCCATATATTT	300			
Db	247	AAGTATTAAGGGCCGCACAAAGCTTTGACAAAGCAATTTGACCTTGAGACTCCATATATTT	306			
QY	301	CAGATCAAGGACCAAGGCGTTGATCAATGTTTCGTTCCATCAATTAAGGGCCCAAGAGCTC	360			
Db	307	CAGATCAAGGACCAAGGCGTTGATCAATGTTTCGTTCCATCAATTAAGGGCCCAAGAGCTC	366			
QY	361	GTTCCCATGACACAGATGAATTTGACCTATACAGTGCCTTGCTAACTTGAATCAACCTGAA	420			
Db	367	GTTCCCATGACACAGATGAATTTGACCTATACAGTGCCTTGCTAACTTGAATCAACCTGAA	426			
QY	421	ATAATGGTAACTTCTAATAGAAACAGAAAATTTCTGSCATCATTAATTTGACCTGCTCATCC	480			
Db	427	ATAATGGTAACTTCTAATAGAAACAGAAAATTTCTGSCATCATTAATTTGACCTGCTCATCC	486			
QY	481	ATACAAGGTTCCCAAGAACCCCAAGAGATGATTTTTGGTAAAAACCGAGAAATTCAGT	540			
Db	487	ATACAAGGTTCCCAAGAACCCCAAGAGATGATTTTTGGTAAAAACCGAGAAATTCAGT	546			
QY	541	ACTAAGTATGATACGTCATGATGAAGAAATCTCAAAATTAATGTCACAGACTCTACAAGCTT	600			
Db	547	ACTAAGTATGATACGTCATGATGAAGAAATCTCAAAATTAATGTCACAGACTCTACAAGCTT	606			
QY	601	TCTATCAGCTTGCTCCTTCAGTCCCTGTAAGCAAGCAATGTGAGCATCTTCTGTGCTCG	660			
Db	607	TCTATCAGCTTGCTCCTTCAGTCCCTGTAAGCAAGCAATGTGAGCATCTTCTGTGCTCG	666			
QY	661	CAACTGTAGTCAATGAAAGCTTCCCTCCTACTTATATATAGATGACACATA	712			
Db	667	CAACTGTAGTCAATGAAAGCTTCCCTCCTACTTATATATAGATGACACACATA	718			
RESULT 6						
LOCUS	PIGCD86G	994 bp	mRNA	linear	MAM 17-JUN-1997	
DEFINITION	Sus scrofa CD86 mRNA, complete cds.					
ACCESSION	L76099					
VERSION	L76099.1 GI:2198558					
KEYWORDS	T cell costimulation.					
SOURCE	pig.					
ORGANISM	Sus scrofa					
	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;					
REFERENCE	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.					
AUTHORS	Meher,S.E., Karmann,K., Min,W., Hughes,C.C., Pober,J.S. and					
	Botchwell,A.L.					
TITLE	Porcine endothelial CD86 is a major costimulator of xenogeneic					
	human T cells: cloning, sequencing, and functional expression in					
	human endothelial cells					
JOURNAL	J. Immunol. 157 (9), 3838-3844 (1996)					
MEDLINE	97047772					
COMMENT	GSDB:S:74002					
FEATURES	location/Qualifiers					
source	1..994					

OY	314	AAGGCTGTATCANTGTTTGGTCATCATATAAAGG9CCAAAGAGACTGGTCCCATGCACC	373
Db	495	AGGGACATATCACGTGCTTCATTATTAAGA6GCCCAAGAGATATGTTCCCATGCACC	554
OY	374	AGATGAATTCAGACTATCAGTGGCTTGCTAACCTTCAGTCAACCTGAAATTAATGGTAACCT	433
Db	555	AAATGAGTTTGACCTATCAGTGGCTTGCTAACCTTCAGTCAACCTGAAATTAACAGTAACCT	614
OY	434	CTAATGACAAGAAAATTTCTGGCATCATAAATTTGAGCTGCTCATTCATPACAGGTTACC	493
Db	615	CTAATGACAAGAAAATTTCTGGCATCATAAATTTGAGCTGCTCATTCATPACAGGTTACC	674
OY	494	CAGAAACCAAGAGAGATGATTTTTTGGAAAAACCGAATTCAGTACTAGTATGATA	553
Db	675	CAGAAACCAAGAGAGATGATTTTTTGGAAAAACCGAATTCAGTACTAGTATGATA	734
OY	554	CTGTCAATGAGAATATCTCAAAATAATGTGCACAGAACTCTACACGTTTCTATCAGCTTGT	613
Db	735	CTGTCAATGAGAATATCTCAAAATAATGTGCACAGAACTCTACACGTTTCTATCAGCTTGT	794
OY	614	CCTTCCTGACCTCCGGAACCAAGCAATGAGACATCTGTGCTCCCTGCAACTGTAGTCAA	673
Db	795	CTTTTTCAGCTCCCTGGAACCAATGAGACATCTGTGCTCCCTGCAACTGTAGTCAA	854
OY	674	T---GAACTTCCTCCCTCCCTACCTTATATATATAGATGCACA--TACGAACCCACACCTCG	727
Db	855	TGAGATATGCTGCTGCTCCCTACCTTTCATATATAGATGCACAACCTTAAGATTAAGACCTCG	914
OY	728	ATGGAGACACATCTCTCGGATGGGGCTGCTGTATGTGTCAITTTGTGTGGGA	787
Db	915	AACAAGGCGACCTCTCTCGGATGGGGCTGCTGTATGTGTCAITTTGTGTGGGA	974
OY	788	TGTTTCTTTCTTAACATAAGAAAGAAAGAAAGAACAGCCTGCCCCCTCATGTGAT	847
Db	975	TGTTTCTTTCTTAACATAAGAAAGAAAGAAAGAACAGCCTGCCCCCTCATGTGAT	1034
OY	848	GTTGAACCAACAAGTAGGAGAGAAAAAGAAAGTAGGACAGACCAAGSAAAGTAGCGGTACC	907
Db	1035	GTTGAACCAACAAGTAGGAGAGAAAAAGAAAGTAGGACAGACCAACAAAGTAGCATCATACC	1094
OY	908	ATGAAACGGAAGATCTATGAGACCCAGCTGTTGTTAACTTTCGAAGACAGTTCAGGGC	967
Db	1095	ACGTACCTGAGAGATCTATGAGACCCAGCTGTTGTTAACTTTCGAAGACAGTTCAGGGC	1154
OY	968	ACAACAGTACTACACAGTTT 987	
Db	1155	ACAACAGTACTACACATTTT 1174	
RESULT 4			
LOCUS	AF157827	1138 bp mRNA linear MAM 08-MAY-2000	
DEFINITION	Felis catus CD86 antigen (CD86) mRNA, complete cds.		
LOCUS	AF157827		
VERSION	AF157827.1 GI:5381423		
KEYWORDS			
SOURCE	Cat.		
ORGANISM	Felis catus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
TITLE	Chol.I.S., Hash.S.M., Winslow,B.J. and Collisson,E.W.		
JOURNAL	Sequence analyses of feline B7 costimulatory molecules		
MEDLINE	Vet. Immunol. Immunopathol. 73 (3-4), 219-231 (2000)		
PUBMED	10713336		
REFERENCE	2 (bases 1 to 1138)		
AUTHORS	Choi,I.-S., Hash,S., Winslow,B.J. and Collisson,E.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JUN-1999) Veterinary Pathobiology, Texas A&M		
FEATURES	University, Bldg. 1197 Rm. 222, College Station, TX 77843, USA		
	Location/Qualifiers		

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	SIOGPEPKFMYPOLMNTSTYKDYPMKSSONVTEVLSIPSEVAHNVSE	
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BASE COUNT	358 a	245 c 246 g 289 t
ORIGIN		
Query Match	78.5%	Score 774.4; DB 4; Length 1138;
Best Local Similarity	88.9%	Pred. No. 1.8e-197;
Matches 861; Conservative	0; Mismatches 101; Indels	6; Gaps 2;
QY	14	GCACATGGAACGTGAATACATCTCTTGTGATGACCCCTCGTCTAATGATGCTGCTT
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QY	74	CCATGAAGAGTCACACATATTTCAACAAGACTCGGAAGACTGCCATGCCATTTTCAAAAT
DB	139	CCATGAAGAGTCACACATATTTCAACAAGACTCGGAAGACTGCCATGCCATTTTCAAACT
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DB	199	CTCAAAACATAAGCTCGATGAGTGTGATGTTTGGACAGGACCGAGATAAGCTGATTC
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DB	259	TGTATGAGATATTCAGAGGCAAGAAACCTCAAAATGTTTCATGCGAAGTAAGGGCC
QY	254	GCACAGGCTTACAAAGACCAATTTGACCCGAGACTGCCATTAATTTGATGATCAAGACA
DB	319	GTCACAGCTTTACAAAGACCAATTTGACCCGAGACTGCCATTAATTTGATGATCAAGACA
QY	314	AGGCGTTGATCAATGTTTCGTTCAATCAATAAGGGCCCAAGAGACTGTTCCCATGACCC
DB	379	AGGCGCATATCACTGTTTCATTCATTAATAAGGGCCCAAGAGACTGTTCCCATGACCC
QY	374	AATATCAATCTGACCTATACAGTGTGCTGTAATTCATGACCAACCTGAATTAATGTAATT
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QY	434	CTAATGAAGACAAATTTCTGGCATCATAAATTTGACCTGCTCATCATCAAGGTTTACC
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DB	559	CAGAACCTAAGAGATGTAATTTTTTCAAGTAAAAACCGAAGATTTCAAGTAAAGTATGATA
QY	554	CTGTATGATGAAGAAATCTCAAAATTAATGTGACAGCACTGACAAAGCTTTCTACACTTGC
DB	619	CTGTATGATGAAGAAATCTCAAAATTAATGTGACAGCACTGACAAAGCTTTCTACACTTGC
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DB	679	CTTTTTCATCCCTGAAGCAGCAATGTGACATCTTGTGTCTGTCGACACTTGAAGTCAA
QY	674	T---T---AAGGTTCCCTCCCTACCTTAATTAATGATGAGCA---TACGAACCCACCCCG
DB	739	TGAGAGTGTGCTCTCCCTACCTTCATTAATGATGAGCAACCTTAAGGTAAGACCCCTG

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 ORIGIN

Query Match 79.7%; Score 786.4; DB 4; Length 1270;
 Best Local Similarity 89.1%; Pred. No. 1.1e-200;
 Matches 873; Conservative 0; Mismatches 101; Indels 6; Gaps 2;

QY 14 GCACTATGAAAGTAATCATCTCTTTGTGATGACCCCTCGCTCTATAGGTCGCTT 73
 Db 256 GCACTATGAGACTGAGTACACACTCTCTGTGTGATGGCCCTCTCTCTCTGCTTCTT 315
 QY 74 CCATGAAGACTCAAGCATATTTCAACAGACTGAGAACTGCCATGCCATTTTACAAT 133
 Db 316 CCATGAAGAGTCAAGCATATTTCAACAGACTGAGAACTGCCATGCCATTTTACAAT 375
 QY 134 CTCAAAACNTAAAGCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 193
 Db 376 CTCAAAACNTAAAGCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 435
 QY 194 TGTACGAGCTATACAGAGGCAAGAACCCCTCAAAATGTTCAATGCAATGTAAGGCC 253
 Db 436 TGTATGAGATATTCAGAGGCAAGAACCCCTCAAAATGTTCAATGTAAGGCC 495
 QY 254 GCACAAAGCTTTGACAAAGCAATTTGACCCCTGAGACTCCATATATTCAGATCAAGACA 313
 Db 496 GTACAAAGCTTTGACAAAGCAATTTGACCCCTGAGACTCCATATGTTACATCAAGACA 555
 QY 314 AGGCGTGTATCAATGTTGCTTCATCATTAAGAGGCCCAAGAGACTCCCTCCATGACAC 373
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 QY 374 AGATGAATTCGACCTATCATGCTTGTATGATGATGATGATGATGATGATGATGATGAT 433
 Db 616 AATGAGTTCGTGACCTATCATGCTTGTATGATGATGATGATGATGATGATGATGATGAT 675
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 Db 676 CTATGAGAACGAAATTTGCGCATATTAATTTGACCTGCTCATTCATCAAGGTTACC 735
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 QY 554 CTGTCTGAGAAATCTCAAAATTAATGTCAGAACTCTACACGTTTCTATCAGCTTGT 613
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 Db 1036 TGTGTCTCTTTCTAAGCTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1095
 QY 848 GTGAAGACCAACAAAGTGGAG 907
 Db 1096 GTGAAGACCAATCAAAAGGAG 1155
 QY 908 ATGAAGAGGAAAGATCTGATGAGAGCCAGTGTGTATGATTTTGAAGAGACAGCTTCAGGCG 967
 Db 1156 AGTACGCTGAGAGATCTGATGAGAGCCAGTGTGTATGATTTTGAAGAGACAGCTTCAGGCG 1215

QY 968 ACAAGACTACTACAGCTTT 987
 Db 1216 ACAAAAGTACTACATTTT 1235

RESULT 3

AY007704

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

gene

CDS

QY 14

Db 195

QY 74

Db 255

QY 134

Db 315

QY 194

Db 375

QY 254

Db 435

QY 435

Db 435

QY 435

Db 435

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Db 435

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ORIGIN		
Query Match	100.0%; Score 987; DB 4; Length 1897;	
Best Local Similarity	100.0%; Pred. No. 1.2e-254;	
Matches 987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGTATCTCAGATGCACTATGGAAGTGAATTAACATTTCTTTGGATGACCCCTGCTC 60
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QY	181	GATAAGCTGGTTCGTGACGAGCTATACAGAGGCAAGAAACCTCAAAATGTTTCATGCG 240
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QY	241	AAGTATAGGGCCGACAGAGCTTGCACAAACACATTTGGACCCGTGAGCTCATATATTT 300
Db	246	AAGTATAGGGCCGACAGAGCTTGCACAAACACATTTGGACCCGTGAGCTCATATATTT 305
QY	301	CAGATCAAGGACCAAGGGCTTGTATCAATGTTTCGTTCAATTAAGGGCCCAAGGACTC 360
Db	306	CAGATCAAGGACCAAGGGCTTGTATCAATGTTTCGTTCAATTAAGGGCCCAAGGACTC 365
QY	361	GTTGCCATGACACAGATGAATTCGACCTATACAGTGTCTGTAACCTTCAGTCAACCTGAA 420
Db	366	GTTGCCATGACACAGATGAATTCGACCTATACAGTGTCTGTAACCTTCAGTCAACCTGAA 425
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Db	486	ATTAAGGTTACCCAGAACCCAGAGAGATGATTTTGGTAAAAACGAGAAATTCAGT 545
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Db	546	ACTAAGTATGATCTGTCATGAAGAAATCTCAAAATAATGTACAGAACTTACAAAGTT 605
QY	601	TCTATACACTGTCCTTCTCAGTCCCTTAAGCAAGCATGTGAGATCTTCTGTCTCG 660
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QY	661	CAACTGGATCAATGAAGTCTCCCTCCCTACCTTTAATATGATGACATACGAAACC	720	
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QY	901	CGGTACCATGAAACCGAAGAATCTCTATGAAGCCCGAGTGTGTAACTTTTCGAAGACAGT	960	
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RESULT 2	AB030652	1270 bp	mRNA linear	MAM 01-MAR-2001
LOCUS	AB030652	Felis catus mRNA for B-lymphocyte activation antigen B7-2 (CD86), complete cds.		
ACCESSION	AB030652	AB030652.1	GI:9796387	
VERSION	AB030652.1	GI:9796387		
KEYWORDS		B-lymphocyte activation antigen B7-2 (CD86).		
SOURCE		Felis catus peripheral blood mononuclear cell cDNA to mRNA.		
ORGANISM		Felis catus		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
AUTHORS		1 (sites)		
TITLE		Nishimura,Y., Shimotojima,M., Miyazawa,T., Sato,E., Nakamura,K., Izumiya,Y., Ikeda,Y., Mikami,T. and Takahashi,E.		
JOURNAL		Molecular cloning of the cDNAs encoding the feline B-lymphocyte activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which interact with human CTLA4-1g		
MEDLINE		Eur.J Immunogenet. 27 (5-6), 427-430 (2000)		
REFERENCE		20465322		
AUTHORS		2 (bases 1 to 1270)		
TITLE		Nishimura,Y.		
JOURNAL		Direct Submission		
COMMENT		Submitted (31-JUL-1999) Yoshiro Nishimura, Faculty of Agriculture, The University of Tokyo, Department of Veterinary Microbiology; 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan		
FEATURES		(E-mail:yoshiro@cirocus.ocn.ne.jp, Tel:+81-3-5841-5396, Fax:+81-3-5841-8184)		
SOURCE		Sequence updated (08-Jun-2000).		
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		/db_xref="gi:9796388"		
		/translation="MGICDPTMGISHTLLIWAALLISGVSSMKSQAYENKGEIPCHFT NSQNSIDELVFWQDDKLVIETIFPKGENPQVHLAKYGRISFDKDNGLRLRHANQ IKDNGTICFLHFKGPKGLVPMQWSSDSLAVANSPQLTIVSNKRTENSGIINVTCS SIOGYPPEKWEQLENTSTPKYKDYVAKSSQNNVTLVYNSISLPSVPEAHNVSVF CALKLETFLEMLSLPFINIDAPKPKDEQGHFLVIAVLVFWVFVCGMVSKTLRKRRK		

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2002, 23:24:30 ; Search time 1351.48 Seconds
(without alignments)
15282.914 Million cell updates/sec

Title: US-09-646-561-9

Perfect score: 987
Sequence: 1 atgatacagatgcactat.....acaacagctactacagttt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_da.*
2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description

1	987	100.0	1897	4	AF106826	AF106826 Canis fam
2	786.4	79.7	1270	4	AB030652	AB030652 Felis cat
3	784.8	79.5	2830	4	AY007704	AY007704 Felis cat
4	774.4	78.5	1138	4	AF157827	AF157827 Felis cat
5	704	71.3	1795	4	AF106827	AF106827 Canis fam
6	620	62.8	994	4	P16CD865	P16CD865 Canis fam
7	620	62.8	994	6	AX027016	AX027016 Sequence
8	575.2	58.3	1002	6	AR147736	AR147736 Sequence
9	575.2	58.3	1002	6	AR159758	AR159758 Sequence
10	575.2	58.3	1002	6	AR160450	AR160450 Sequence
11	575.2	58.3	1112	9	HUM872A	L25259 Human CTLA4
12	575.2	58.3	1120	6	AR030780	AR030780 Sequence
13	575.2	58.3	1120	6	AR112747	AR112747 Sequence
14	575.2	58.3	1120	6	AR146413	AR146413 Sequence
15	575.2	58.3	1120	6	AX047043	AX047043 Sequence
16	575.2	58.3	1161	6	AR146414	AR146414 Sequence
17	570.2	57.8	1424	6	AX330924	AX330924 Sequence
18	570.2	57.8	1424	6	AX332506	AX332506 Sequence
19	570.2	57.8	1424	6	HSU04343	U04343 Human CD86
20	570.2	57.8	2205	6	AX188198	AX188198 Sequence
21	565.2	57.3	972	6	AX027005	AX027005 Sequence
22	561.6	56.9	1048	9	AF344857	AF344857 Macaca mu
23	560.6	56.8	1062	9	AF344861	AF344861 Cercopit
24	554.2	56.1	1062	9	AF344840	AF344840 Cercopit
25	552.6	56.0	1044	9	AF344851	AF344851 Macaca ne
26	537.2	54.4	1156	4	RABCD86B	D49842 Rabbit mRNA
27	466.8	47.3	924	4	BT4291475	AJ291475 Bos tauru
28	463.8	47.0	751	6	AR147737	AR147737 Sequence
29	463.8	47.0	751	6	AR159759	AR159759 Sequence
30	463.8	47.0	751	6	AR160451	AR160451 Sequence
31	453.8	46.0	738	6	AX002781	AX002781 Sequence
32	453.8	46.0	738	6	AX149548	AX149548 Sequence
33	447.2	45.3	901	9	AF344836	AF344836 Papio cyn
34	344.4	34.9	930	6	AX027012	AX027012 Sequence
35	344.4	34.9	984	10	AF065897	AF065897 Mus muscu
36	344.4	34.9	984	10	AF065898	AF065898 Mus muscu
37	344.4	34.9	984	10	AF065899	AF065899 Mus muscu
38	344.4	34.9	984	10	AF065900	AF065900 Mus muscu
39	344.4	34.9	1115	10	S70108	S70108 early T cel
40	344.4	34.9	1151	6	AR030781	AR030781 Sequence
41	344.4	34.9	1151	6	AR146412	AR146412 Sequence
42	344.4	34.9	1163	6	AR112764	AR112764 Sequence
43	344.4	34.9	1183	10	M05B72X	L25606 Murine B7-2
44	339.6	34.4	2528	10	BC013807	BC013807 Mus muscu
45	337.2	34.2	1261	6	AR146408	AR146408 Sequence

ALIGNMENTS

RESULT 1
AF106826 1897 bp mRNA, linear MAY 14-DEC-1999
LOCUS Canis familiaris B7-2 protein (CD86) mRNA, complete cds.
DEFINITION AF106826
ACCESSION AF106826
VERSION AF106826.1 GI:6572516
KEYWORDS
SOURCE
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1897)
AUTHORS Yang, S. and Sim, G.-K.
TITLE New forms of dog CD80 and CD86 transcripts that encode secreted B7 molecules
JOURNAL Immunogenetics 50 (5-6), 349-353 (1999)
MEDLINE 20093996
REFERENCE 2 (bases 1 to 1897)
AUTHORS Yang, S. and Sim, G.-K.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Basic Immunology, Heska Corporation, 1825 Sharp Point Drive, Fort Collins, CO 80525, USA
FEATURES
Location/Qualifiers